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<p>(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW</p> <p>(57) Abstract</p> <p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>		

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HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

5 Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may
10 contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

15 There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is
20 primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed
25 mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon
30 genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence
35 reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.

A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogeneous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

- (a) preparing a mixture comprising a heterogeneous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;
- (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;
- (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and
- (d) carrying out an extension synthesis in the mixture produced in step (c).

Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

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Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually, therefore, all DNA species will be present at the same concentration.

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The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for each DNA population.

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In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

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In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogeneous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid population is treated by:

(a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adapted cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

(c) selecting and separating only those adapted cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok I.

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin reaction in selecting and separating desired adapted molecules. Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adapted molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adapted end of the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adapting" process can be used to generate categories or subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

- (a) a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- (c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that
5 when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or
10 sequence in accordance with the invention may be released by the endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

15 Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

20 Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA
25 fragment is in operable reading frame with a control or regulatory sequence.

Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved
30 using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

35 Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and
40 Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other
10 methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

15 It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate
20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate
25 indication of where the beginnings and ends of the component sequences are.

In contrast to investigations hitherto, where gene fragments (sequence fragments) could only be identified through some known characteristic
30 [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by
35 functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior
40 art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alessio, J. M., et al., Focus (Gibco B.R.L) 9 p1 (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltzfuz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher

eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. Gene 40 p183 1985), Shimuzu, Y et al., Gene 65, p141 (1988), Straus, D. and Gilbert, W. Proc. Natl. Acad. Sci. 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith, D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. Nature 353 pp605-607 (1991), Rudensky, A., Y., et al., Nature 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable, although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., Proc. Natl. Acad. Sci. 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide. Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase (Nagai, K., and Thogersen, H., C. Methods Enzymol. 153 p461-481 (1987)). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

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All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 (1985)).

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Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age fetuses and then snap frozen in liquid nitrogen before storing in bijou bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA⁺ (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983)) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

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instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

The column eluate was adjusted to 10 mM Mg^{2+} and then the purified cDNA was restricted by the action of 1 unit per 10 μ l of the endonuclease Pst I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

The adaptors used were oligonucleotides 5' N,N,N,N,TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTGCGAGGAGAAGGA (SEQ ID: 1195) and 5' AAN,N,TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' TTN,N,TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added $MgCl_2$ to 10mM, ATP to 10mM and 0.025 units/ μ l of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume was 90 μ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

The column eluate was adjusted to 25mM Mg^{2+} , 0.5mM dNTPs in a final volume of 200 μ l. The mixture was placed in a thermocycler (Technique MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200 μ l of streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400µl each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg²⁺. The beads were then resuspended in 240 µl of the final buffer including additionally 0.5 mM dNTPs and divided into 4x60
10 µl.

Four of the 60 µl aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adapted fragments. 2 pmoles of the primer 5' CTGTCTGTCCGAGAGAAGGAA
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTCCGAGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes
20 and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 µl of resuspended beads were added to each reaction to remove the
25 biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an
30 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one
35 of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCACTGTCCGAGAC (SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8 μ l or 12.5 % whichever was the larger but not exceeding 12 μ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM Mg^{2+} , 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40 μ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60 μ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75 μ l or 75 % of the column eluate, whichever was least, were added 9.5 μ l of 100mM TrisHCl pH7.4, 100 mM $MgCl_2$, and 9.5 μ l of 0.5 mM dTTP. 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptor the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptor were performed according to standard procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C, respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive. In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40µl reactions containing 2.5mM Mg²⁺, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic workstation attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluorescein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the above procedure.

Example 2

A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTGACAAGCTTGAATTCGGGCCGC(T)₂, (SEQ ID: 1210) was used at 1 μ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5 μ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100 μ l with water.

PCRs were then performed in reactions containing 1 μ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl₂, 0.01% gelatin, 200 μ M dNTPs, 10 uCi ³²P dCTP, 1 μ M each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

5

cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyosarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15

Clear plaques from each library were resuspended in 5 μ l of Tris-HCl pH 8, 1 mM EDTA. 2 μ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30

Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

35

The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

21

(1) GENERAL INFORMATION

(i) APPLICANT

(A) NAME: MEDICAL RESEARCH COUNCIL

5 (B) STREET: 20 PARK CRESCENT

(C) CITY: LONDON

(E) COUNTRY: ENGLAND

(F) POSTAL CODE: W1N 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

(iv) COMPUTER READABLE FORM:

15

(A) MEDIUM TYPE: DISKETTE

(B) COMPUTER: IBM PC COMPATIBLE

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: EXTRACT

20

(2) INFORMATION FOR SEQ ID :1:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1:

	GCCGATTCGT GACCAAGAAG GCTCTGTGCA TTCGGGTTTT CCAGGAGACT	50
35	CAAAGCTGA AGAAGCGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA	100
	ATAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTC CAAAGCCATAC	150
	CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT	200
40	GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAT ATATCATATA	250

22

TATATATATA CACA

264

(2) INFORMATION FOR SEQ ID :2:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15 AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT 50
GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC 100
CTGGGGAGGG GGTCATTGTT CTCT 124

20

(2) INFORMATION FOR SEQ ID :3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC 50
35 TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC 100
TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAACGA ACTGAGATGC 150
AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA 200
40 GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA 250

23

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG 300

TCACATATTA GGAAGTATA ACATAAGGTA AAC 333

5 (2) INFORMATION FOR SEQ ID :4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC 50

GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTCT GTCTTTATGT 100

20 AAGAAGAAAC TGCCTAGATG ACGGGGCTC CTCTTCAA CAGGAATTTC 150

TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCC CTGCCCCCAT 200

25 (2) INFORMATION FOR SEQ ID :5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA 50

AGATTGCCA AATTGTAGCC TACTGGATTC CGGTTCTCTT GACATCTCTT 100

40 TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA 150

24

ATTAAAAAAA GGGAGGATTT AAGAATAATG AAAAGAGAAA AATCAAGAAA 200

GCACAATCAC TAG 213

5 (2) INFORMATION FOR SEQ ID :6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG 50

GAAGTTTAA GCTAAGATT GCCAAATTGT AGCCTACTGG ATTCCGGTTC 100

20 TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACTTCCC GAGTATAAAC 150

GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG 200

25 AAAAATCAAG AAAGCACAAT CACTAGTGTA GAGATAACAG AATTTCTGAA 250

TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT 300

GTGGCCCATATA CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC 345

30

(2) INFORMATION FOR SEQ ID :7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

TCCATTTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50
GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100
5 GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT 150
TTCTTTTCC 159

(2) INFORMATION FOR SEQ ID :8:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20

ATATTTCAAT CGAACAAAA GGAACTTTT TTTGAACTTA TTGAGGCTCT 50
ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCCT 100
25 TGCCTGGCTG GGGGTTTGAT TCGC 124

(2) INFORMATION FOR SEQ ID :9:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :9:

CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA 50
40 TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG 100

26

ACCGGGATGC AGTGTCAAGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG 150
GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCTGTTC 200
5 CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA 250
GAAAATAGA 259

(2) INFORMATION FOR SEQ ID :10:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCCAGGG CCCTCAAGAA 50
GCTCCTGCAC ACAATAAACG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT 100
25 CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA 150
GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA 200
CTGTGACAAG GGGCCC 216

30

(2) INFORMATION FOR SEQ ID :11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :11:

27

CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG 50
CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCCTGTA 100
5 AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT 150
GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG 200
GGATG 205

10

(2) INFORMATION FOR SEQ ID :12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC 50
25 AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT 100
CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA 150
GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CTTTCTTGGG 200
30 TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA 250
TATGCCATTG TCGGTGA 267

35

(2) INFORMATION FOR SEQ ID :13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :13:

5 GCCTCATCAG GTTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50
GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG 100
CAATGTGAAG CTGAAC 116

10 (2) INFORMATION FOR SEQ ID :14:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTGGTCTC TTCGTATGGT CAAACTTCAA 50
CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG 100
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT 150
ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACTCTA 200
30 AGGGGTGCAA GGACCAGGCT TTGATTTCOA ATTATAATCT AATGCTCACT 250
CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

35 (2) INFORMATION FOR SEQ ID :15:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :15:

	CGTCAGTGTG CTACTTCACA TCATTAGCGA GGCCCAGAAA CTTGAACAGG	50
5	AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC	100
	CAAACTCGAT TCAAAGAGCA ATA	123

(2) INFORMATION FOR SEQ ID :16:

10

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| | (A) LENGTH: 262 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 15 | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20

	CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT	50
	GGCATTGTCA GAAAAATTTA ACAGGTTTAT TTATAATTAT CATAAAGTTG	100
25	ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCAATTA ATGCTTTACG	150
	TCTCCGCATT TATATTAAAA ATTCACACAC AAATGAAATG GAAAAACTGC	200
	CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA	250
30	CTTTTGACTC TA	262

(2) INFORMATION FOR SEQ ID :17:

35

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| | (A) LENGTH: 169 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 40 | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :17:

5 TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG 50
AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT 100
TGAAAGTAAG TTTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATTT 150
TCAAGAAACG TGCATCAGC 169

10

(2) INFORMATION FOR SEQ ID :18:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :18:

AGGGGCACCA TTACCATCCA TCTGACATCG CATTTCATA GAAATGGCCA 50
25 AAGAAAGAAG GTCCTGGTAG GTTTTTCATA GAAAGACTCA AAAAGTTCAA 100
CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA 150
TTATTAAAAT ACTGGCTTCG GTTTCITTTT TTCCTTTGCA AAGTTTCCTA 200
30 CATATATGTC TTTTACAGTA T 221

(2) INFORMATION FOR SEQ ID :19:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

31

(xi) SEQUENCE DESCRIPTION: SEQ ID :19:

5 TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA 50
TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT 100
TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC 135

(2) INFORMATION FOR SEQ ID :20:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20

GTTATCTATC TATCTTGCAG TTTACCTATC TGATCTGATC TCTGTAATTA 50
TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTT TACATTTCAA 100
25 AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG 150
TTATTTTCA GAATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT 200
TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTA AAAAAATTGT 250
30 ATAATTTTGT GATAATGTAG TTTCCCAAAA CACATTTAGA AAGCATTATG 300
TTATTAGTAA ATGA 314

35

(2) INFORMATION FOR SEQ ID :21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :21:

5 TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT 50
TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC 100
TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT 150
10 TCCTCTTTCA ATATTTCTGT TTCTTGCC 178

(2) INFORMATION FOR SEQ ID :22:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID :22:

ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT 50
25 ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGACAGAA 100
GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTTT 150
30 TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT 188

(2) INFORMATION FOR SEQ ID :23:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 40

33

(xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNTCNTTTAN TGCTTTTATA TTTTNNAAAT 50
5 GTTAAAACCC CTATACCACC TTTTGGGAAT GTTTTAAATT CTCCAATTTT 100
TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTTATCA ATTGAATTGA 150
GG 152
10

(2) INFORMATION FOR SEQ ID :24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :24:

ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTTCA 50
25 ACTTTTGCAC ACTTTTCAA CGGTCCCACC ACA 83

(2) INFORMATION FOR SEQ ID :25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :25:

AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA 50
40 ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT 100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAC CATNTGCACC 150

CTACATCTGG CTGACATTTA CATTTT 176

5 (2) INFORMATION FOR SEQ ID :26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACGCTTT TAAAATATTT GAACAGAAAA 50

GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC 100

20 TTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150

TTAAGTACTG ACGAAGAAGA CTAAACAAT CATTTTTTAA CAATATTAA 200

25 AAGGATCATA TAGTCGACTT TTAAACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG 50

40 GCCCAATCTT CCCAAGTCCA CACAGGAGGG AAACATTGTT TGCGTAAATA 100

35

CGCAATGCAA AATTNNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTTCG 150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT 100

20 GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 T 201

(2) INFORMATION FOR SEQ ID :29:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTTCAC TTTATTGGCC 50

40 CCTCCCTACA TTCGGGTTAG GTTCCATTG ATTTGCACAA TAATGACTTT 100

36

ATTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTA TCATAGAACT 150
AACTATTTA ATTACATATA ATGTAATAA TGGAGAGATT TATAGAGAAT 200
5 TTTGTTTTT TGTCATATAC TCCATTTTGA AGACAGATAT GATAGAACTA 250
GAAATTAAGT TGCATTTCTG CAACT 275

(2) INFORMATION FOR SEQ ID :30:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20

GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC 50
ATTCATCAAC AAGATTTTGA ATGGAATATT CCAGAAATTT CTGAGCCATC 100
25 TGATCACAAC AACCGTCTTT GA 122

(2) INFORMATION FOR SEQ ID :31:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :31:

40

GGATTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT 50
AGAGATCTTC CCAATGAACC TCAATACACG ATCGTAATAC TCGCACAATG 100

37

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC 150

TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCAAT GTGAAAC 197

5 (2) INFORMATION FOR SEQ ID :32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG 50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC 97

20

(2) INFORMATION FOR SEQ ID :33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA 50

35 CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT 100

AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC 150

AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC 200

40

CTAGGAAAAA ATAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT 250

CACATAAGA

260

(2) INFORMATION FOR SEQ ID :34:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15 GGACNTGCGC NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG 50
ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT 100
GATCCAAAAT ACCTTCCTTN CCAAGCCCGG GGTNNNGAT AAGGTGTGGA 150
20 NTTNGGTAA AGACAAGG 168

(2) INFORMATION FOR SEQ ID :35:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35 CTCGNACACT GTGGAGAGCC TCGNNNNNN NNGGTNTACT CAGGGGGACG 50
AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT 100
GCTNNNGTGG TCCCTTAGNA CCCGAGNAGG TGGGCGCGAG GTGAANAAGG 150
40 TGCNNGTGCG AGAGTGCGTG ATT 173

39

(2) INFORMATION FOR SEQ ID :36:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA 50
15 CAACTAATAA TGATTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA 100
GTTTGTCTAA CCTTGTAAG CTGTTTACC GTT 134

(2) INFORMATION FOR SEQ ID :37:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :37:

30

TGGCGCCTGT CCGAGAGCAA GTNGNNNNN NNCCTGAAAG TCAAAATGGA 50
ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTGCTC AGTACAGACN 100
35 GATTACAAT GAAAGTTTTG CTAACCTTGG TAAGCTTGTT AACCGTTTAC 150
ATGACTTCTT 160

(2) INFORMATION FOR SEQ ID :38:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :38:

CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAAATCCCA CCCTCACACG 50
ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT 100
CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC 140

15

(2) INFORMATION FOR SEQ ID :39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :39:

AGCAAGTATC ANNNNNNNNN ATACATTTGA ATTCAAGTTG TTTTGTGTC 50
AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG 100
GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG 150
CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAAAN NATTANGGGA 200
AAA 203

35

(2) INFORMATION FOR SEQ ID :40:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

41

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

5 GAAAAGCNNN NNNNNNNGGC TTAAAGAACA ATATGCTGAG ATGGAGAAGG 50
10 ACCTAGCGAA ANTNNNAACC TTTTAAGAAC TTGAANNACA ACAATCACAA 100
15 ACTAATGAGA AGATGTTTAC CTCTCTCCTG AAAACTATGC CCACCAGACC 150
20 GTTTAGCCTC TGCTCAAGCT 170

15 (2) INFORMATION FOR SEQ ID :41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

30 GCTGCATGTT TCCTTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA 50
35 AAAAGGGAGC CAATACAGAT CTTCCTCAATG AACCTCAAAC ACGTCGTAAT 100
40 ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA 150
45 CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA 200
50 ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG 250
55 AAATTTGATT TGTAATAAAA 270

(2) INFORMATION FOR SEQ ID :42:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

42

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :42:

AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC 50
CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT 100
AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC 150
ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT 200
GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA 245

20

(2) INFORMATION FOR SEQ ID :43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :43:

TACACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC 50
TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA 100
ATGAAGACAC TTTACTTTT TCGG 124

(2) INFORMATION FOR SEQ ID :44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

43

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG 50
GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA 100
AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA 144

(2) INFORMATION FOR SEQ ID :45:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25 ACTGATTCNN NNTGAAAATA CCCCCTTTCT CCATTAGTGG CATGCTCATT 50
CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTTTAA 100
CAAAAAAAAA AACAAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA 150
30 GAAATTTAAT GTTTTTCATA ACATGAA 177

(2) INFORMATION FOR SEQ ID :46:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :46:

ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT 50
5 TTATCTTTAT ATTCAAATAA GTTATTTCGC TTCACTGTT TTAACAAAAA 100
AAAAAAAAA AAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT 150
TAATTCACAC GGAAAAACCA AGACAATTTC ACAACTTCTG GACACAACCA 200
10 TCAACACAGG ACATTTTTTT TACAGGCAAA TCACTTAAAA CAAAAAAGAT 250
CCCAGA 256

15 (2) INFORMATION FOR SEQ ID :47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

GAGAAAAGTC NNNNNNNNA GGTAAATCTA ACTTTTCTTG CTTATTTTCTAG 50
CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTTT 100
30 AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG 150
AGCAA 155

35 (2) INFORMATION FOR SEQ ID :48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5 GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAATGAT GAATAAGATA 50
TTTNNACAAA GATACACG 68

(2) INFORMATION FOR SEQ ID :49:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :49:

20 CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG 50
GGCCTAGCTA AATTTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA 100
ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC 150
25 TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG 200
AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG 244

30 (2) INFORMATION FOR SEQ ID :50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

ACTCGNNCAG CGATAGTCGG AGCTCACCAA CAAAAACNCT NNNNCAGAAA 50

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

(2) INFORMATION FOR SEQ ID :51:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15

GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA

50

AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAT

100

20

TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT

150

TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT

200

TTATACCAGA AGNATGACCA CTG

223

25

(2) INFORMATION FOR SEQ ID :52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTTNT TGTAAGAAAG CTCANNNANA AAGGGANNNGG CTTAAGAGA

49

(2) INFORMATION FOR SEQ ID :53:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

47

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :53:

CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA 50
TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT 100
TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA 150
TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA 200
TTCAATAATC AAA 213

20

(2) INFORMATION FOR SEQ ID :54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :54:

30

GCGTGTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG 50
CGTNNTTGGC TANGGGGNGG GTTTNGGCAG GTGTTGCCGG TAGCNAAACN 100
GTGGGCCCCA TNGCCNGNAT TGNNNCCCN CNNGGGAANG GGGGGGGNGA 150
CCNNAGNGGG AAAAAA 166

35

(2) INFORMATION FOR SEQ ID :55:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :55:

ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT 50
NGNCGTTGTN GCTGCCAAGC GACAT 75

(2) INFORMATION FOR SEQ ID :56:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :56:

AATNNNNNCC TATTTTGTA TTTTGTGAA AAAAGTTCAA TGTTCAAGTTT 50
TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA 100
AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA 150
TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A 181

(2) INFORMATION FOR SEQ ID :57:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

49

(xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA 50
5 GATGACGNNNA TCCAATTTC A GAACACCACA GGGCACTGGC ACACAGAGGG 100
GATTATTACA GAACCACTGA GATGACATTT 130

(2) INFORMATION FOR SEQ ID :58:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20

GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA 50
CATTGACAAG TACAAAAATT AAAAAATAT GCAGAAATAT TGAATAACTA 100
25 GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT 150
CCATGAA 157

(2) INFORMATION FOR SEQ ID :59:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40

GAGGTGAAGT TGTTCTTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT 100
GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATTT 150
5 TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200
AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250
CA 252

10

(2) INFORMATION FOR SEQ ID :60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50
25 GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100
AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTTCAACTT 150
TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:

51

GAGGTGGCAT TATGTGAGAC AGCATTGGT TAGGGAGTGC CAAGCATTCT 50
ACAGCATTG ATGGTGGAA TAGTCATGCT TTTATTTCT GCTCTCTAGG 100
5 AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAGGTC 150
CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA 200
GAGTGCTTCT CATAACCTT CAGGAACCC 229

10

(2) INFORMATION FOR SEQ ID :62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :62:

CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAA GGGACTGAAG 50
25 AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA 100
ACCGCTTAAT GAATTTTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGGC 150
AAGAGCTTTT GGA CTGTTT TAGAACAGAA T 181

30

(2) INFORMATION FOR SEQ ID :63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :63:

52

5 GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA 50
ATTTGGCAGA AACAGAAAA GGACATGGGA TAACTTTTAG ATTTAAAGAG 100
GCAGGCTTGG AACACAACT GGTATTCTGC TGACACACTG CTGCATATCA 150
TAAGGCTACT CCACAAGACC ATTAGAAGTC 180

(2) INFORMATION FOR SEQ ID :64:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :64:

20

ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC 50
AGGGAAGTGT GATTATTTAA AAATANGCNA GAACTTATT CANCTGTGCT 100
TTAGAAANAA NTGTATACGG 120

25

(2) INFORMATION FOR SEQ ID :65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :65:

CACATCGCTA TAATCCTTTC TGAGGACTTA AAACCTTATN CCACTTACCT 50
TTATGACTTT TAACAAGCCT 70

40

53

(2) INFORMATION FOR SEQ ID :66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :66:

TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT 50
ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG 100
GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC 150
CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN 200
TCCACACACC CACACGATTT AGGAACTTGG ACATGTTTCCT 240

(2) INFORMATION FOR SEQ ID :67:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :67:

GGAAGCACTA CATTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT 50
TACGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT 100
TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT 150
AACCTATTTT TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG 200

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250

TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAAGT GAAAGACTAA CCAAGATTG 50

ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100

20 TCAACAAATN NNNACAACG AGAACCTGGG AATTCCCGCA CGGAAGACAA 150

GAGATAACCT CTCCAATTTA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNAAA CAAAAGACAG GAGCAGAGAG GCCTGAGAGC 50

40 AGGAGGCGAA TTCGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC 100

CCGGGGGAAG CC 112

55

(2) INFORMATION FOR SEQ ID :70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTTAATCC TTGGGTGTT TTACCACTTC TTTCGTAAAT 50
TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG 100
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT 150
ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG 200
CAGATTTATT CCTTTAACTG ACATTTCCAT GA 232

(2) INFORMATION FOR SEQ ID :71:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :71:

CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT 50
TTCACCTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG 100
GAACCTTTGA GGAGATCGAC TGAAAGACTA GCGNCCCNGT CAGATAAGAT 150
TTAGGGCTGA 160

56

(2) INFORMATION FOR SEQ ID :72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT GGTTCGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC 50
AATACGTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT 100
CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGAAGT TTCGATTCTT 150
TTTCCTCCC GTCGCAAATT CTATGTTTGG AT 182

20

(2) INFORMATION FOR SEQ ID :73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG 50
ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA 100
CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG 150
ANAGGCTGCA CAATGAAA 168

40

(2) INFORMATION FOR SEQ ID :74:

57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC 50
AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCAGGGTT 100
GTATACCACA CCCCAGGGCCC CTAATCCCAG GCCCGGAGAT AGGAAAGCCA 150
ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC 200
NCTNTCCCTN NAATAAATTN C 221

20

(2) INFORMATION FOR SEQ ID :75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGCATCCGA GATCATTAAA AATGNCTGAC CCTAACAATA 50
GGCACAAAAA TAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT 100
TAGAAAAAAA CAGGGCCTTG AGTTCTG 127

35

(2) INFORMATION FOR SEQ ID :76:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :76:

10	AAAAGAACAG CAGTTTCACA TTTACATAT TTGAAAACA TTTCAAACC	50
	CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAAAGACC	100
	ACAAAATTAA TACTACCAAA TCATTACTGA GACTCTTGCA TTACAATATT	150
15	TGGAGAGTAG GTGAAGAAAA TTAGACCGA	180

(2) INFORMATION FOR SEQ ID :77:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 142 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :77:

30	GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC	50
	GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAACTG	100
	TCACTTTAGC CNCNAACTAC AAGACCNGTT AGACTAGAGA GC	142

(2) INFORMATION FOR SEQ ID :78:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 40 | (A) LENGTH: 124 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :78:

5 GGCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC 50
ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT 100
CTGNCCCCCC CNNGNCCCC CCG 124

(2) INFORMATION FOR SEQ ID :79:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :79:

20 AGGTATAGTG TTCCTAATC ATGTA CTGTG GAAGCACCCG GANTTTTTCA 50
TATAGTCTAA AAGCTAGAAG AACAAGAGTG TATTTCGTGG GTGGATGTAT 100
25 NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT 150
TTAAGNAAAN GCCNTTTTAA G 171

(2) INFORMATION FOR SEQ ID :80:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 98 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :80:

40 CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA 50

60

CGACACTGCC GTGNGGGCAC CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR SEQ ID :81:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15

CCTCAACAAG TCGGAGACCT GGGCGTCCAA CCTGCCTACA ACCACAGCCG

50

CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT

100

CAACATCA

108

20

(2) INFORMATION FOR SEQ ID :82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC

50

35

CCTCAATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA

100

GAATGTCCCA TCACAGTCTT CCGTCAAAAT TTAGCCTCAC AACAACAACA

150

ACGCCTACGA AATTCTAAAT TCAGAAGGAA

180

40

(2) INFORMATION FOR SEQ ID :83:

61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT 50
CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC 100
GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC 150
CTTCTTAATA AACACCTCCT CGCCAACTGC GACGACCACA ATCACCGTA 199

(2) INFORMATION FOR SEQ ID :84:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA 50
CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA 100
GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG 150
CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATTT 200
NACNGAATAC AACC 214

40

(2) INFORMATION FOR SEQ ID :85:

62

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10 CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC 50
AGTACCTGGG CATGTCCTGT GATGGCCCCCT 80

15 (2) INFORMATION FOR SEQ ID :86:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :86:

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC 50
CCTGAAATAC GCGCTTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT 100
30 CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT 150
GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTTA TTACTCTGTT 200
35 TCTTTTAATG 210

(2) INFORMATION FOR SEQ ID :87:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

63

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT 50
ATTTAAAAAT ACTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA 100
CA 102

(2) INFORMATION FOR SEQ ID :88:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25 GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT 50
ACGGGCGAGT AGAACATTAT CTGTATAACA GGAAGTGTGA TTATTTAAAA 100
ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA 150
30 TAAGTTGAAA AGAACTCAAA ATAATAATA CAAATAAGAA CCTACGTATT 200
AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250
35 TGACACAAAT TCAAAACAG ATCAT 275

(2) INFORMATION FOR SEQ ID :89:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA 50
TTAATAGTAA TTATGGTTTG GNNGTAAAT CGAGTTTCAG AATAAAATNA 100
10 AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAGCT TTTGTTTTGT 150
TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTTC 200
15 TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT 250
GCTGTGTACT CCA 263

20 (2) INFORMATION FOR SEQ ID :90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :90:

GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC 50
CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCC CGAGGGACCC 100
35 CTTTGAGA 108

(2) INFORMATION FOR SEQ ID :91:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

65

(D). TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :91:

	GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT	50
	ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA	100
10	TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTCAG AGCACCACAG	150
	GGCACTGTGT ACACATGAGG GGTTACCTTA CAGAGCCACT GAGAATATAT	200
15	TAATAA	206

(2) INFORMATION FOR SEQ ID :92:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 210 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

	CCTTGGTGGA GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA	50
30	TGGCTTTGGC TGATAGATT GAAGAGACCT CAATTACGTT TTTCAGGAAT	100
	GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG	150
35	GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT	200
	AATAAANNNG	210

(2) INFORMATION FOR SEQ ID :93:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 189 base pairs

66

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :93:

AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAACT AACCTAAAAG	50
GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA	100
AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGCTCCTGT	150
GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG	189

(2) INFORMATION FOR SEQ ID :94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :94:

GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTGTAA ACTAACCAAG	50
CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC	100
TCAACGCATG ACAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN	150
GTCATTTAAT	160

(2) INFORMATION FOR SEQ ID :95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

67

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT 50
AAAAGGCAAC AATTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT 100
AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTTT 150
TAAGGAAACT ACAGAAGGGA T 171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT 50
TTCCCAACC TTTTATTCG CGAAGAACT CCAGTTGTTA ACTTTTGTAG 100
30 AGTTTTTTTT GGCAAAAGAA CTNCATTAN C 131

(2) INFORMATION FOR SEQ ID :97:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

68

(xi) SEQUENCE DESCRIPTION: SEQ ID :97:

5 GTCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA 50
 GTAAAGTTAA GGCCTGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA 100
 CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN 150
 TTAAGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC 200
 10 ATAATGTATT GATGATCTGC TGTAACCTTG AGAAGCTTCC TGAAGCTCNT 250
 TTTGAATAAA TTTATNGAAC TTATGAAGA 279

(2) INFORMATION FOR SEQ ID :98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :98:

25 GTGAGTCTTT CTTCAACTAG GGAATGTTT CCAGGGCAGC CCAGGCCTCA 50
 CTCACGCAGG CCTCCGCGAC AACTGTTCAG CACTGACTGA GGATGAAGTG 100
 30 AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA 150
 CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT 200
 35 GACGAGACCA GGACCCTTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA 250
 AACTCCAGGG CCTCCA 266

(2) INFORMATION FOR SEQ ID :99:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs

69

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA 50
10 ACAAATAGTA AAACACATA GAGTAATGAT TCATTTTGGT AAAAAATATA 100
TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA 150
15 GTGCTTACCC CTGGGAAGGG GGTATACGAT GTTGATTAC TCTTTGGGTA 200
CGTATT 206

(2) INFORMATION FOR SEQ ID :100:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

30

CGCAACTNTC NCTAAACATC CAGTTTTCTA ATNTAATAAA AAATGGCAGT 50
AATTATCCTC ACCTCTCAGG GAA 73

35

(2) INFORMATION FOR SEQ ID :101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :101:

5 GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50
ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT 100
ACTGCCCC 108

(2) INFORMATION FOR SEQ ID :102:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :102:

20 GAATTATCAA ACCATCNTTG CTGACATTAA TTTTCCAGCT TTGATCTTAN 50
NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTCTCA AACGATNTAT 100
25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150
TCAATATAAC ANAAAAAGGN ATTTTGCAAA AAGTACAAGT TTTATGTCTN 200
30 CTGTAACTG 210

(2) INFORMATION FOR SEQ ID :103:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT 50

GTCACCAAAA TTTCTTTCCA AAAAAA 76

5 (2) INFORMATION FOR SEQ ID :104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAAA TCTTTCATAG AAAGATATTA TCAAAGCTGA 50

AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA 100

20 CCGATTGAAT GGTTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC 150

AAGTCGCAAG GAACATC 167

25 (2) INFORMATION FOR SEQ ID :105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC 50

CTCACGGGAC CACCATCATA CAGCAATTTG TCATGATCAA AAGAAACATC 100

40 ATTAGTCGTG CCATAACTGT AT 122

72

(2) INFORMATION FOR SEQ ID :106:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCTTCA CTCCAGATT CCAATGCCAA GATACATTGA TACTGAACAT 50
15 GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCAACCC TCACAGACTC 100
ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA 150
GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG 200
20 TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA 250
AATAA 255

25

(2) INFORMATION FOR SEQ ID :107:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGAATA TTTACAAAGA AACTGTTTT CTCAAAACAC 50
TGTTCAATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA 100
40 AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT 150

73

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT 200
ATACCAAGAN ACANTTATGT GGTAAAT 227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTTNNNN NGCCATACCA TGGTACAATA 50
ATCATNAAAA NACAANAACA AAAACAAACA CATAAACCA CTCACATATA 100
20 CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAAAA ATAGNAAAAA 150
AAAAAAATAA CA 162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA 50
AAATAAAAAA CGAAACCCGA GAACCAAAAT GAACGAAAAT CTTTCGCTTC 100
40 ATTCATCGTC CCCACAATNC CAGGCCTACC CCCCATACTG ATCATTCAAT 150

GTTT

154

(2) INFORMATION FOR SEQ ID :110:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15 ATGTGCCAAG TAAAAAATCA ATNGTNGCC TTTTCCATT NCGCGGACAC 50
CCATAGGCAC CAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG 100
AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT 150
20 GCACTCCTTG TTAATAACAA TACACTATAT CA 182

(2) INFORMATION FOR SEQ ID :111:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35 GAAGGTGAGA ATAGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA 50
CNTCAAACC AATGGTAGAA CATCACATTT CAACTGCAA ACCA 94

(2) INFORMATION FOR SEQ ID :112:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs

75

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10 TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT 50
GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT 92

(2) INFORMATION FOR SEQ ID :113:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25 GATTGTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG 50
TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG 100
ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAACTCCAA GAATCTAGAG 150
30 GG 152

(2) INFORMATION FOR SEQ ID :114:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

76

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTCAGTG 50
5 TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG 100
GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA 150
TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA 182

10

(2) INFORMATION FOR SEQ ID :115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :115:

GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC 50
25 TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC 100
AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC 150
TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT 182

30

(2) INFORMATION FOR SEQ ID :116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :116:

77

GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTG ATAAANTAAC 50
ATACAAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA 100
5 TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT 150
ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAA CACGTAGTGA 200
TGGAAATAAG CTAGCTACGC TCAATGC 227

10

(2) INFORMATION FOR SEQ ID :117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :117:

CGAGAGATTG GTAATGAGGA AGCAATTTGG AGGGGNGGAA GCTACAANGA 50
25 NNNNGGGAAT TACAACAATC AGTCTTCAAA TTTTGGACCC ATGAAGGGAG 100
GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC 150
TTGCAAAACC ACGAAACCAG GT 172

30

(2) INFORMATION FOR SEQ ID :118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

78

AATGATGGAA GCAATTTTGG AGGTGGTGGA AGCTACAATG ATTTTGGAAAT 50
TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG 100
5 GCAGAAGCTC TGCCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG 150
AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG 200
GCAGAAGATT 210

10

(2) INFORMATION FOR SEQ ID :119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT 50
25 TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC 95

(2) INFORMATION FOR SEQ ID :120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

GGAGTATTTN AANNTTTCAA ACTTTATTAC TTAATGAAAC AGTTTCTATA 50
40 TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTTTTTG 100

79

TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTTT ATTAACGCT 150
TCCAGAAACC GTAACAGG 168

5 (2) INFORMATION FOR SEQ ID :121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTTA TCTTTCAAAC TCCNTACTNA GTGAAACAGT TTCTATACCA 50
CTGCTTCCAA TTACTANCTN TTTTNTCNGT TAAATTTTCN NCTGTTTTTC 100
20 AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA 150
ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA 200
25 ATACATACTT CGGTGACNTT ATGCATCATG A 231

(2) INFORMATION FOR SEQ ID :122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT 50
40 AGCTGTTTAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG 100

80

ACACCATTGT ACGGTCTACA ATGTCATGGG ATCAGGTGTT CAAACTGATT 150

GGAATCTTTC TGAAAAGGAT ATGA 174

5 (2) INFORMATION FOR SEQ ID :123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAAATG TTCTGTTATC 50

AACTGNNTTT ATAAAAAATC GATTGTGGGT AGAAGCAGAG AAAAGGCACT 100

20 TAGTAAAGAT ACTACATGAN GAAAAANNTC TGCCCTTGA ATTCTTANGA 150

AACATNNTNG NNGAATCAAT 170

25 (2) INFORMATION FOR SEQ ID :124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNTTATAAA 50

AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACTTAGTA AAGATACTAC 100

40 ATGANGAAAA ANNTCTGCC TTTGAATTCT TANGAAACAT NNTNGNNGAA 150

81

TCAATNT

157

(2) INFORMATION FOR SEQ ID :125:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15 CAACTTGAAA TACATTATGA TGTCTGATAT GATTAAATAT CATTGAGNAT 50
CTTGCAAACA AAAAAAGCAA AAAATTAAAT CTCCATATCA ATCTTAAATT 100
CTTGGCATAT TTACTTCTGG TAAATATTAC TTCTGGTCCT TATTCTATAT 150
20 GTGTTATTGA AATTGTGTT 169

(2) INFORMATION FOR SEQ ID :126:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35 GTTTNGTTNN NNNNTGTTCC ACCTTTTGTT GAATTTTAGT TGTTAGGCTG 50
AACCTCCGAG CAGTTTNAGG ACTTGCCTGA GTTTTCTTC 90

(2) INFORMATION FOR SEQ ID :127:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG 50
10 AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTTCA CCACTTGACA 100
TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT 150
15 AGGAAAACCA 160

(2) INFORMATION FOR SEQ ID :128:

- (i) SEQUENCE CHARACTERISTICS:
 - 20 (A) LENGTH: 150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :128:

CCCCACAAC TACATCCTCA TTATTGGCGC CTACAACTC AACTACGAAC 50
30 AACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTACTCGGCT 100
ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC 150

35 (2) INFORMATION FOR SEQ ID :129:

- (i) SEQUENCE CHARACTERISTICS:
 - 40 (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :129:

5 AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTCCGAAG 50
CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA 100
GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA 150
10 TGAAAAACCC AAAACAGTTA CGANGCTAAT CC 182

(2) INFORMATION FOR SEQ ID :130:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :130:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50
25 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC 100
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150
30 TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA 200
TGCTTACTTC AAGAAGAAG 219

(2) INFORMATION FOR SEQ ID :131:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

84

(xi) SEQUENCE DESCRIPTION: SEQ ID :131:

ATAAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAA 50
5 GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT 100
CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCITTTGTAGT 150
AGAACATCGT TAACGGAATC ACAGATATAT C 181

10

(2) INFORMATION FOR SEQ ID :132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT 50
25 GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG 100
TAGAAGATGN AAACAACTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG 150
CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC 188

30

(2) INFORMATION FOR SEQ ID :133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :133:

85

GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC 50
TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGAATTTCAGT 100
5 CACGACTGAG TTGATGGTGA CTTGACCTGA GAGATTTTAC AGAAGCTCTG 150
TGAATTGGTT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC 190

(2) INFORMATION FOR SEQ ID :134:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20

ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC 50
AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC 100
25 CAGGGTCCAT TTAAC TAAGA GGTGGTGATC TCCACGCCAG CCCC AAAGAT 150
GTCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA 200
TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG 235

30

(2) INFORMATION FOR SEQ ID :135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

86

GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT 50
ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC 100
5 AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG 147

(2) INFORMATION FOR SEQ ID :136:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :136:

GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA 50
20 CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG 100
NTCCCANTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA 150
25 CTNAGAATGC GGAGGAGATC T 171

(2) INFORMATION FOR SEQ ID :137:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :137:

ACATATATGT GGTAGGATAG AGAGATGGNN NNNGTGTATG ACATAGGTGT 50
40 TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATG 100

87

TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTGAGTCT 150
GTAAGTAGG 159

5 (2) INFORMATION FOR SEQ ID :138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAATA AAACACGAC 50
NCACTCACA TCGCTCATAA TCTCTNAGG ACTTCAAAT NTCTCTNTGA 100
20 NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCNTGTNC 150
TNCGGGAGAA CTCTCTGTGC TGTACCAGT 179

25 (2) INFORMATION FOR SEQ ID :139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC 50
TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG 100
40 ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA 150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

(2) INFORMATION FOR SEQ ID :140:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTGTGA 50
CTTATACTGT CTNTGTCAGT TA 72

(2) INFORMATION FOR SEQ ID :141:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30 GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTTA AGTATTNGTT 50
TTAGTACGNA AA 62

(2) INFORMATION FOR SEQ ID :142:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5 ACCAGTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT 50
GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTTTA AGAAAACGAG 100
TTAAGTTTAA CAGTTTGTCA TTACAGG 127

(2) INFORMATION FOR SEQ ID :143:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :143:

20 AATATAAAAG ACAGCAGTTT CACATTTTAC ATATTGAAA AACATTTCAA 50
AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT 100
25 GACCACAAAA TTAATACTAC CAAATCATT CTGAGACTTT TTGCATTACA 150
ATATTGAGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATTT 198

(2) INFORMATION FOR SEQ ID :144:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :144:

40 GTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA 50

90

AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG 100
TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG 150
5 AAACTGCTTT GTATCTGCTT TGNA 174

(2) INFORMATION FOR SEQ ID :145:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :145:

GAGAAATAGT ACTTTAAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT 50
20 AAGATTCATA AAATGTACCT TTTTGTATTG TTTTGTTCN GAGTTTTCGA 100
TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA 150
25 TTTTGG 156

(2) INFORMATION FOR SEQ ID :146:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :146:

AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50
40 GTTGGAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100

91

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT 150

T 151

5 (2) INFORMATION FOR SEQ ID :147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAAGTC 50

CAGGTAANNT GGTTCGATCT GATCGATTG GCTGCATACT TTCGGTACGT 100

20 ATAACATTCT AAAGTTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG 150

TAAAATTTTA AAAGTTAAAG TACTAGC 177

25 (2) INFORMATION FOR SEQ ID :148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT 50

TGGAAATTGG CTGTTTGTG AAAATATATC TTTAGTGTG CTTTAAAGTA 100

40 GATAGTATAC TTTACATTTA TAAAAAAAT CAAATTTTGT TCTTTAAT 148

(2) INFORMATION FOR SEQ ID :149:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50
15 GTTGGAATTT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100
TAGATAGTAT ACTTTACATT TATAAAAAA ATCAAATTTT GTTCTTTATT 150
TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA 200
20 ATCC 204

(2) INFORMATION FOR SEQ ID :150:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :150:

35 AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATGAATAGGA 50
TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT 93

(2) INFORMATION FOR SEQ ID :151:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :151:

10 AATCGAGAGA AAAAATGATG AACTGTAGC AATATCGTCG GANTCCACCT 50
ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC 100
CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAC CAGGAAGGTG 150
15 T 151

(2) INFORMATION FOR SEQ ID :152:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :152:

30 TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT 50
CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA 100
TGTAGCCTC 109

35 (2) INFORMATION FOR SEQ ID :153:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :153:

5 AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50
TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100
AGGAAAAGGG GAAAAAACC CATAATGGGC CTAAAA 136

(2) INFORMATION FOR SEQ ID :154:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50
CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100
25 TCAAGATGAG TATACGCATC TATCATTCGA ATTGTGTCAT TAATTTGTAG 150
GGCCTCATTG 160

30 (2) INFORMATION FOR SEQ ID :155:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

ACCAGTNNNN NNNGGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA 50

95

ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTTNCT TNTCTCCTTT 100
TTTTAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT 150
5 GACTTCATGC TTA CTGTAAA GTGGAAGTTG AGATATTTTA A 191

(2) INFORMATION FOR SEQ ID :156:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :156:

CAACTGAACG CTTTGGTCAG GCTGCTACAA TGAAGGAAT TGNGGGCNAN 50
20 TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT 100
GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCACTG 139

25 (2) INFORMATION FOR SEQ ID :157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :157:

GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA 50
CCAATACTAA AAATTATATA AGATGTGCAC AATTNNNNGC AGGCAATCTT 100
40 TCTTTTGTTT ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA 150

96

AGCACCCGCA AATTACCTT TG

172

(2) INFORMATION FOR SEQ ID :158:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15 GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT 50
CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG 93

(2) INFORMATION FOR SEQ ID :159:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30

GNATTTTTTT ATTGATATAT CATAGTTGTA CAAACATTG GGAGTNCANG 50
TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC 100
35 CA 102

(2) INFORMATION FOR SEQ ID :160:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

97

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

GCTTTTNNNN NNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA 50
TAGAAGCAAT AANNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT 100
10 ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT 150
ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA 200
15 GCGGA 205

(2) INFORMATION FOR SEQ ID :161:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA 50
30 AGTTGTTTTTC CATATAAAAA ANNNNNNTGA TTTTAAAAA ACTAANNAAC 100
TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAAGTGG GNCACCAAAA 150

35 (2) INFORMATION FOR SEQ ID :162:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :162:

5 TATTCAAAAG AAAAACATGG GTAAAAATGA TAGTGTTAA TCTTGGCTCT 50
GTGTACATAG ATAGATACCT GTTACAG 77

(2) INFORMATION FOR SEQ ID :163:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :163:

20 GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT 50
TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT 100
AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTCT 150
25 CAAACTGACA TGCTACAGAA ATGTCTTCCA AA 182

(2) INFORMATION FOR SEQ ID :164:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :164:

40 GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA 50
TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC 100

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT 150

CAGATTCACA GACATTGCA AACAGAAGA TG 182

5 (2) INFORMATION FOR SEQ ID :165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAATAC TAGGAATACT TATTCTATAT 50

GAGACATATA TACCACCCAA GTTTTAACAC CATATCCCAT CGGCTGTTAG 100

20 TGTATATAAA AAGAAATAA 119

(2) INFORMATION FOR SEQ ID :166:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTCC AAACACATAG 50

GATCCCATCT CAGGAGCAGG ACCAGTGTTC AGCTAGATTA AACTTCGCTG 100

40 GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA 150

AGATGTTATG GCAGAAGTGA CTTGTTTTGC TCAACAAGCA TTG 193

100

(2) INFORMATION FOR SEQ ID :167:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG 50
15 GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT 100
GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT 150
TAAATGGACA GTTTATAAAG TGGTCTGGP GCCGA 185

20

(2) INFORMATION FOR SEQ ID :168:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG 50
35 TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG 100
ATTTCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA 150
ATTTTAAAA ATA 163

40

(2) INFORMATION FOR SEQ ID :169:

101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10

AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTCAGATG CCACCGTATA 50
GCAAAGGGTG AACATGTTTT CAACCCTTTA ACTTTTACG GTGTTTGAAG 100
ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG 150
CAGATTTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC 200
CT 202

20

(2) INFORMATION FOR SEQ ID :170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :170:

TCAGGGAACC AAAAACTGG CTTGCTTGGC ACCCAGGGAC AGTAGCTGTT 50
TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC 100
ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT 150
GGTGCCCGAG GCTGTAAA 168

40

(2) INFORMATION FOR SEQ ID :171:

102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10

AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA 50

GCAATTTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC 100

15

TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT 144

(2) INFORMATION FOR SEQ ID :172:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :172:

30

ACCCACAGNN NNNACCTAGA GGCCAGCGC CCAGAGAGGC ACGTAGAAAT 50

GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A 91

(2) INFORMATION FOR SEQ ID :173:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

103

(xi) SEQUENCE DESCRIPTION: SEQ ID :173:

	GATTTTTTAA TGGGTNGCCT CTTTtagCTT GGAATATTAC GTTTACTTTA	50
5	ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT	100
	GAATCCCTTT GACATCTATT ACAGGTATA GGACCTTTTT GGTGTGATTA	150
	CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTTGGCA GAAGTTAAAA	200
10	TGGA	204

(2) INFORMATION FOR SEQ ID :174:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 241 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :174:

25	GTAAATTCA CTACATCTTT TNNTNGACT TTCATGCATT TCTCATACAT	50
	TNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTAA	100
	ACGAAAGGCG GTTCAATTCA TCAACTTGAA ATGACTATTT ATTTTNNAGG	150
30	ATTTTTTAGG GGAAGAGTAC CCATTTCGTT TATAAAAACA GATGACAAAT	200
	TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G	241

(2) INFORMATION FOR SEQ ID :175:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 211 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

104

(xi) SEQUENCE DESCRIPTION: SEQ ID :175:

5 GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT 50
TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT 100
AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC 150
10 TTACAGGTTT CTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT 200
TTGGCCCTTT T 211

(2) INFORMATION FOR SEQ ID :176:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25

AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG 50
NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN 100
30 TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA 150
AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTCTT GACCTATGAT 200
AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA 250
35 AT 252

(2) INFORMATION FOR SEQ ID :177:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid

105

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

	GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA	50
10	GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG	100
	TTGCAGCCAA TCTTCTCAA GCAAACCGAC TTCCTAACAA CTNTCTACAT	150
15	CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA	200
	TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC	250
	ATCTGAAGAT ACCAGCTTCA AATACTAAT	279

20

(2) INFORMATION FOR SEQ ID :178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :178:

	TATGCCCTGA AATGAAACCT CTAAGTTTGA CAAAATACCC AAAAAACAG	50
	ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTG GTGGGTGGTC	100
35	GTTCTCAATT TATAAANAA TAAATGACTT TAAAGGAGAA ATAAATTTAT	150
	GTCAGGA	157

40

(2) INFORMATION FOR SEQ ID :179:

(i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10 GATAATGCAA CTTTGTACAG GAAAGCGCGA TTTTACTAT 39

(2) INFORMATION FOR SEQ ID :180:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

GCAAACTCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG 50

25 GACTTAACT CTACTACACT AATACTTTTT GATGACTTCT AACAGCCTC 100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG 150

30 TACCACA 157

(2) INFORMATION FOR SEQ ID :181:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:

107

CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA 50
CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC 100
5 ATTCTGGTAA AAACCTGGAAG ATGACCCTAA ATTTTGAAGT TGATGATGTG 150
CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT 195

(2) INFORMATION FOR SEQ ID :182:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20

CATGGTCTTA ACCAGTGTCA GATGGAATCA GTGGATAAAT CCCCAGGTTT 50
GTTTGCCTT CAAATGGGAC AATTGAGGA ATGCTTTAGG CAGAGGACTC 100
25 AGATGACAGA GCGCCAACCA CCCACAATAG AAACCTGCTC ATCACA 146

(2) INFORMATION FOR SEQ ID :183:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :183:

TAGAGGAATA GGGNNNGNGA CGCCCCNAGT TGTAGGGACG GACGGAGGAC 50
40

(2) INFORMATION FOR SEQ ID :184:

108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10

ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC 50
AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG 100
CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAGAT 150
GTCCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA 200
TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT 248

20

(2) INFORMATION FOR SEQ ID :185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :185:

AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT 50
ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTTG 100
AACGTGGCTT TCT 113

35

(2) INFORMATION FOR SEQ ID :186:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs

109

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTCC CAGGATCCCG 50
10 ATGTCGTCAT ACACTCCGAA CATGACCCCTT TTTCTTTCCA ACGATCAACC 100
ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC 148

15 (2) INFORMATION FOR SEQ ID :187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :187:

TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG 50
TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA 100
30 GCCAACTACA CTCCCACTGC TAAAAAGATG AAAGGACCAA TCAAAGATTT 150
AATTAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC 200
35 TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC 248

(2) INFORMATION FOR SEQ ID :188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTTCA 50

GTTTAATACA TAAGTGCCA ATAATAATGT CAACCCTCCC TCGCCACAGC 100

10

CAATAATTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT 146

(2) INFORMATION FOR SEQ ID :189:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25 ATTTACCACA AGGGACGATT TCCACACCAA CCCC AAAAAT GTCCCCTATG 50

ACGACGAAAT GTGTATTGA AACAGCTCTG A 81

(2) INFORMATION FOR SEQ ID :190:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

40

AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA 50

111

GAGCAAGAAT TGAAGATGCA CAAACTTCCT TCTGAATTG TGAGCTTCCT 100

GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA 50

ATGGGGCATA CGAGTAATAT GTACATATCA AACAATCAAT TGCCTCCTGA 100

20 AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTTAGGCCAA 150

CA 152

25 (2) INFORMATION FOR SEQ ID :192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTTGAT TCGGTAGTAA GGTAAGACG ATTTTATAGA 50

ATNAAGGTGA TTCCT 65

40

(2) INFORMATION FOR SEQ ID :193:

112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2 ? base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10

AGGACCCAAA CTACCTTATT GCATTGGAAG TTTTACTTAT NCTATTATAA 50

TCTAAGAGCC CACCCAACAA GGCACTACAC ATAGATGCTC ACACTCTATA 100

15

GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG 150

CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC 200

TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA 249

20

(2) INFORMATION FOR SEQ ID :194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :194:

GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG 50

35

TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC 100

GCTGCATATG TGA CTGTCAT GAGATCCTAC TAGATGATCC TGA CTAGAAT 150

GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT 194

40

(2) INFORMATION FOR SEQ ID :195:

113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10

GTGATTTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA 50
TTTAAGTCAC ACACATAGTT AACACNCNC GTNGCGTGCA ATAAATACCA 100
CATCCTTTNA TATGNNCNGN A 121

15

(2) INFORMATION FOR SEQ ID :196:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :196:

30

GGGCTTCNNN NNNNNNCATG TGCACCTAGA ACCGTTACTA ACCGAAACAC 50
CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT 100
AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA 150
TTGTGACCAC AAGTCTTGTT TCTTG 175

35

(2) INFORMATION FOR SEQ ID :197:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :197:

ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG 50
AATCAGAGGT ATCAATGAAA TGAGCCCCAAA GGTTCGAAAG CTCGCAACTT 100
10 CTTACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT 150
ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA 200
15 AATGACTAAT CTACAAGCNT GTTATGCAA ATAAATAAGA AACGACTTGC 250
TTACAGATGC NTTTAATTG TGG 273

20 (2) INFORMATION FOR SEQ ID :198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT 50
GNTATA 56

35 (2) INFORMATION FOR SEQ ID :199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

115

(xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5 GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG 50
GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC 100
CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA 132

10 (2) INFORMATION FOR SEQ ID :200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :200:

AAACTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC 50
GACATTTCOA TCGNACACAA ANTAAAAAA TAAACAAAT TTAAAAAAC 100
25 CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAATTCOA 150
GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG 200
30 CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN 250
TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT 284

(2) INFORMATION FOR SEQ ID :201:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

116

(xi) SEQUENCE DESCRIPTION: SEQ ID :201:

	CCTGACACCA ATTCGCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA	50
5	AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTNT	100
	CTTGNT	106

(2) INFORMATION FOR SEQ ID :202:

10

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| | (A) LENGTH: 270 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 15 | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20

	CTTTGAAAA CAAACATTN TTATTACTGA AATAGCAAAA ATCATTCTAC	50
	ACTCCTCCTA AGCATGTTCA ATTAGCATAC ATTCCAACAA TGCATGAAAA	100
25	AATTNCTAGC CAGAGGCATT TAAGTGATTT CTCCTAAGT GTTTGCTAAT	150
	TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA	200
	CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT	250
30	CATTACTCTA ACTGTTAATC	270

(2) INFORMATION FOR SEQ ID :203:

35

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| | (A) LENGTH: 173 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| 40 | (D) TOPOLOGY: linear |

117

(xi) SEQUENCE DESCRIPTION: SEQ ID :203:

AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA 50
5 AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA 100
ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAACTG ATTTTACTT 150
TACAAAANNG NAATTGCAA TTA 173

10

(2) INFORMATION FOR SEQ ID :204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :204:

CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN 50
25 ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT 100
CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT 150
CATTAAACATT ANTT 164

30

(2) INFORMATION FOR SEQ ID :205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50

AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC 50

ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100

20 TGGGGTTAGN TGTTCNAA 118

(2) INFORMATION FOR SEQ ID :207:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACAATT AAAAGNCTNC TCACACAAGN ATCTTTTTTAA 50

TAAAAATACC TCTTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCTG 100

AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150

40 GCTATGCATA ATACCCTCAC 170

119

(2) INFORMATION FOR SEQ ID :208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA TGCTTGATA CAATGATATA ACAAAGAAAC CCTAAGACAA 50
CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATTT 100
TTTCTCGGGG AAGTAACCCCT GCCTTTGAA 129

(2) INFORMATION FOR SEQ ID :209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :209:

CTTGCGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG 50
GATCCTTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT 100
CCAAATTTTG GCTCCAGAGT CATTTCTGAA NNTCTACACT TANGGNCTTN 150
AGCNTGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT 190

(2) INFORMATION FOR SEQ ID :210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs

120

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

TCATTGAGTC ATCCTTTTTG CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG 50
TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT 100
GATGCAGAAC TGTTTCATAT CTAGAAATG 129

15 (2) INFORMATION FOR SEQ ID :211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG 50
CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG 100
AAATGGAANC NNNGNGTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT 150
GG 152

35 (2) INFORMATION FOR SEQ ID :212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

121

(xi) SEQUENCE DESCRIPTION: SEQ ID :212:

CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG 50
5 TCGAAAGATG AAAACAATA AGTTCATAAC CCCCTGCCCC CCATTGACCT 100
CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTACATC 150
10 NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT 186

(2) INFORMATION FOR SEQ ID :213:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :213:

CTTAAATGCC TGTTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA 50
25 CCTTTCTCTA AAATTCCTTT CCTTTGCCTC CTCCTCTAAC TTTTCCTCCT 100
TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTTG CTTCACTCTA 150
30 TT 152

(2) INFORMATION FOR SEQ ID :214:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

TC TTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG 50
ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACTC CCACCGTATG 100
5 TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC 150
ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT 200
GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT 250
10 ATTATTCAAT AGTGGAATG ATGACTACAG CTATACCTCA 290

(2) INFORMATION FOR SEQ ID :215:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25 GTTCTTCCA GTACATCCAA GTTTAAATT ATTAGCGAAA TGGTCCATGT 50
TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGAAGATCT 100
GAGAGCATGC TGTTTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC 150
30 TGGGCCTCAC TTTACCCCAT TCGTAAATG GGGATAATGT CACCTGCCTC 200
TTACCTACCT CAGAGGGATT TGCGAAGCAA ACTGTTAATC TTCGAAAACG 250
35 ACCATTTACT TTTAGGATAT CAA 273

(2) INFORMATION FOR SEQ ID :216:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT AGGGAGAAAC AATGTTCTTA CATATTATGG GTAGTGAGAA 50

CATTATCTGT ATAACAGGGA ACTGTGATTA TTTAAAATTA TGCAGAACTT 100

10

ATTTTCATCTG TGCTTTAG 118

(2) INFORMATION FOR SEQ ID :217:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25 GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAGAAGA AAACAAGTCT 50

ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTCACGAAA CCCTTTTAAA 100

TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAATAAA NGNNNTGATT 150

30

TACCACCAAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA 197

(2) INFORMATION FOR SEQ ID :218:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218:

CTCGCGAGCA CTCGTCCGAG AGGTCCCATTA C>NNNNNNNCC CAAGCCCCTC 50
5 AAGGGCCTTT GCCAATCTNG TCATTTTATG CCAAGTCCTC TAAACGCAC 100
TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC 150
TATTTTAGGC TNCNAGGTCA AAATAAA 177

10

(2) INFORMATION FOR SEQ ID :219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :219:

GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA 50
25 GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAAG 100
TNGGTNTCAG GGCTGGAC 118

30

(2) INFORMATION FOR SEQ ID :220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :220:

GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTTT 50

125

ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAACTGTA 100
CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT 150
5 TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN 200
NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA 233

(2) INFORMATION FOR SEQ ID :221:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20

GCACACAGAT ACCATCCCAC CTTGCTTNT GACAGGCCAG CCACACAATA 50
ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA 100
25 GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA 150
CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAAACCTG 200
TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT 235

30

(2) INFORMATION FOR SEQ ID :222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

	GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG	50
	CCTTAGGAAT TGANTGAGGA CTAAATTTC CCCNGAGGGA GAGNAGTGGA	100
5	G	101

(2) INFORMATION FOR SEQ ID :223:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :223:

	ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC	50
20	ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT	100
	TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT	150
25	TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA	200
	ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC	250
	CATTCTTGAG ATACCAGCTT C	271

(2) INFORMATION FOR SEQ ID :224:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE. DESCRIPTION: SEQ ID :224:

127

AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA 50
ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA 100
5 T 101

(2) INFORMATION FOR SEQ ID :225:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :225:

TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT 50
20 AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA 100
GACCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTTCA A 141

25 (2) INFORMATION FOR SEQ ID :226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :226:

ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG 50
TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG 100
40 TTCTGTTATG TGCAAAGTAG ATTATTTTCAT ATTTACTTGG TATGGAAAGC 150

128

AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200
AAAANGCTGT TNNAAAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAACTTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNGGTGG 50
TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG 100
20 CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT 150
TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG 200
25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50
40 ANCATTTTCG CCAGAATGGT GTAATGNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTTT TTTTAAATG GTAAAACCCC 150

TTTTTACTGG NCNTTCCAGA ANCTTACAG 179

5 (2) INFORMATION FOR SEQ ID :229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCACAAGT TATTGTAGCA GTGAAACAAT 50

GAGGGCATAC ACTATATNGA AAAAAAACC TCCTCCCTNA TTCTCAGCC 100

20 AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGTTAA 150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA 184

25 (2) INFORMATION FOR SEQ ID :230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTC 50

TTTTTAGGTT TAGAATTTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTTA 100

40 GTGCAACAT TGTGAGTAT GTTGTCAAAC GTCTAAAAAA 140

130

(2) INFORMATION FOR SEQ ID :231:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT 50
15 CCTAAGGCAG GAAGATGGTG GCNNNTNNGG ACGAAAAAGT CGCTGGNGNN 100
NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG 150
GGGGTAAAAG NAANATNNGA ANATGGAT 178

20

(2) INFORMATION FOR SEQ ID :232:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC 50
35 CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT 100
NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATTT TATANCTTCN 150
NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG 200
40 GCAACCANGG 210

131

(2) INFORMATION FOR SEQ ID :233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :233:

	ACTGTGCGAG TAGCTTNAAA ANNNNNNNNN NNACTCAGTT TNATTATAC	50
15	AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC	100
	CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG	150
	ACTNTCTNAC NTTCAAACNA NTATTNCAG TAAAAACAT CACAGTGCGA	200
20	AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG	247

(2) INFORMATION FOR SEQ ID :234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :234:

35	AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT	50
	GTGGACATTG GAATGTTTAC TGTATTCTG TGTAAGAAAA CAACTNACAA	100
	AAAAGAAAAA TGGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC	150
40	NGGGGGAAAN TGCCNGGGC	169

132

(2) INFORMATION FOR SEQ ID :235:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA 50
15 G 51

(2) INFORMATION FOR SEQ ID :236:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTA AAA TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC 50
30 TCAAACTTTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA 100
A 101

35

(2) INFORMATION FOR SEQ ID :237:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

133

(xi) SEQUENCE DESCRIPTION: SEQ ID :237:

5 CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG 50
ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA 100
CAGTTTTCCA GCAGTTTTCG TATTNTTTT TATTACGAA TGCCATACTC 150
10 TGTTTT 156

(2) INFORMATION FOR SEQ ID :238:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :238:

GCAGNCTAAT TGTGAATCTA AGAACTACT CATAGACATC CCACCCTAAT 50
25 GATTTTACCT NNAACNTTG TCCTTCATCA TAGAACCTA GCAACATCCA 100
CCTCCTGTAG CAGGAAACGA ATCAAACAAC CCCCTGGATA ACCTCTCA 148

30 (2) INFORMATION FOR SEQ ID :239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :239:

GAGTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA 50

134

AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA 100
AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA 150
5 TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTTT TCCACTAAGG 200
CCCTTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA 250
TCTTCTCT 258

10

(2) INFORMATION FOR SEQ ID :240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA 50
25 CAAACCAGTG ATTCCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG 100
GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA 150
CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT 200
30 TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG 250
CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC 300
35 AAGGGTNAAC NTNTTNNAA ANNNGCCNAA NCNNGATTTT GNACNCCCTT 350
TNNCATTGGC ATTNANTGAA AAAAGTT 377

40

(2) INFORMATION FOR SEQ ID :241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

135

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

GGNGCACTGN TCCGAGAGCT TTTTNTCTG AAGAATAGCA TCTTTAATGA 50
GTGTNCTAAT CCTTGTCTATC TGAAGTTTGG AAATATATTT CCCAGGGTCA 100
GAACAATACA GAGA 114

15

(2) INFORMATION FOR SEQ ID :242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :242:

CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTTNN CCATTAAAAA 50
GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA 100
AAAAAANCNA AAGNGGGCCC CC 122

30

(2) INFORMATION FOR SEQ ID :243:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

136

(xi) SEQUENCE DESCRIPTION: SEQ ID :243:

50
GAGAATGGGA AGCCTCATT TGGGGACAAG AACCTGTACA AGGATTGTG
5 ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC 100
NTATGATATG CCTCATGATA TTNTGCATC TGAAGATGGG ACTNTGTACA 150
TTGGNGATGC TCATCCAAAC C 171

(2) INFORMATION FOR SEQ ID :244:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :244:

50
AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT
25 TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAAA GTTAAACAG 100
GACTTTCAAC TTAATCCAGA CTCCTAACA GTGTTTACAT GTGAGGGAAA 150
CTCCTTTAAG TAATGCGTAG TGTATTATTT TTACCATCAT TGGNGACAAA 200
30 AAAAACAAAA ACATAAACAT CTNANGTGAA ATATA 235

(2) INFORMATION FOR SEQ ID :245:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

137

(xi) SEQUENCE DESCRIPTION: SEQ ID :245:

GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG 50
5 TCTAAGTTAA AAACGCCCTG CCCCCTTCTC GCAGGCCACC TACACCGTNN 100
TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCTGC 150
NTNTACNTCT AACCNAAACA TNACNGCGGC CACCTACTCA TGCCCTANTG 200
10 CAGCNCACCC T 211

(2) INFORMATION FOR SEQ ID :246:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :246:

25 GGCTGAGAAT CCTTGAGCTT ACCATTTGAT ATTTCTATAT TATTTAAGAA 50
AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT 100
ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT 150
30 GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA 194

(2) INFORMATION FOR SEQ ID :247:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

5 GACCTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG 100
CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT 150
GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA 200
10 GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT 249

(2) INFORMATION FOR SEQ ID :248:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :248:

25 GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT 50
GACCTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG 100
CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT 150
30 GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA 200
GCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC 248

35 (2) INFORMATION FOR SEQ ID :249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

139

(xi) SEQUENCE DESCRIPTION: SEQ ID :249:

5 GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTGCGCTTG 50
GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA 82

(2) INFORMATION FOR SEQ ID :250:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20 GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG 50
TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAACCAGN 100
GAGAGATGCA CAAGATTAC AGGCC 125

(2) INFORMATION FOR SEQ ID :251:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :251:

GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG 50
40 AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAA AGCGCGTTTT 100
TCTGGGGGAG CGGCCGCCTT TAGTCGACCC 130

140

(2) INFORMATION FOR SEQ ID :252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :252:

GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA 50
AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT 100
TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT 150
ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGTTTTT 200
ATGNGATAAT ATCAGC 216

(2) INFORMATION FOR SEQ ID :253:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :253:

GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTAAAAAATT 50
ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTCCTT CCAAAGAAGN 100
TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA 150
TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT 200

141

TTTTCAGAAG GATCTTTTGT AGCAGTGNNT ATGAATGNAC CCGCAAAT

249

(2) INFORMATION FOR SEQ ID :254:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15

GACCCCATTC TATATTATNC GTNNNGCGAT TTTTAGCCA CCCTGAAGTT

50

ATATTTNTAT ACCNAGGCTT CGAATAATCT CATNGACTN ACCACCCTNG

100

20

GAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG

150

CTCCCTGGGN TTCTTG

166

(2) INFORMATION FOR SEQ ID :255:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35

CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTCAA GAGCATCTGG

50

AACACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA

100

40

AGATTTGCTC GCTGAGAAAG TCCTTGTGGG AAATCGAAGT TGAGGACTAC

150

TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC

200

142

CTTCTNTTGT NACAGACAGC AGA

223

(2) INFORMATION FOR SEQ ID :256:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15 GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT 50
TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC 100
TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA 150
20 CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC 200
CTGACGATCT TTCCCTAGAT CATTCTGACC TGTGTAGAG TTGTTGAAGG 250
25 AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC 292

(2) INFORMATION FOR SEQ ID :257:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :257:

40 AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT 50
AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG 100

143

ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT 150
GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCTGACGA 200
5 TCTTTCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT 238

(2) INFORMATION FOR SEQ ID :258:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :258:

GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA 50
20 GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG 100
AACCGGCTCC AAGCATTCGT CACAGCACTA ATTTAAA 137

25 (2) INFORMATION FOR SEQ ID :259:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :259:

GCGCGACTTT TAAGGGATTT GCNGTGATGC CTGTTGACCC AGTGCCTTCC 50
TAGCCGGGAA GGGGCTCGGC TGGAGTGNN AAGGCTCAGAA AAATTTCGCG 100
40 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

144

TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTT CGTGTTACAT 200
CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTTT AAGGGATTG CNGTGATGCC TGTGACCCA GTGCCTTCCT 50
AGCCGGGGAA GGGGCTCGGC TGGAGTGNN AAGGCTCAGA AAAATTGCG 100
20 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150
TTTTGGACAG GTGGGGCGGT GACCTTGGA TGTATTTTC GTGTACATC 200
25 GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50
40 CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT 100

145

ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC 150
ACTTCCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT 200
5 GATCCCTGGA TAAACAGGAT CATTTCAAAG NNGTTTATA 239

(2) INFORMATION FOR SEQ ID :262:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :262:

GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTGTGTA AACAGCCATT 50
20 GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG 100
TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA 143

25 (2) INFORMATION FOR SEQ ID :263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :263:

GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCCTGTAA TACCTCCTCC 50
TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC 100
40 TAAAAAATA TAGCAATCCA CATAGGCTTC GATTTCCTGT GACACTCTGA 150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT 200

TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT 50

CTGTGTTAAA TCGTATGCTT TTAAAGGTA TTAAAGATT CAACTAGCTT 100

20 TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG 150

ACCTGATCTT GATGTTCTGC TGTGTNAGT CTTGAAGAGC GATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT 50

TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA 100

40 AAACAGCTGC CTTCTGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150

147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCCC TCCAAACAGG 200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGGAAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG 50

TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACTCG CGTTGTCATC 100

TCCCAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC 150

40 AGGGTGGAGG CAGATGTCT 169

148

(2) INFORMATION FOR SEQ ID :268:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG 50
15 GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG 100
CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT 150
20 ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAACA AGTGCTGCCT 200

(2) INFORMATION FOR SEQ ID :269:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGGCC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG 50
35 ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC 100
TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCTT GAATTGTAAA 150
CACTAAGTGT AGT 163

40

(2) INFORMATION FOR SEQ ID :270:

149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :270:

10

TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG 50
GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA 100
CCACTTATTC TTTCT 115

15

(2) INFORMATION FOR SEQ ID :271:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :271:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNGGN 100
NCCATTATNG NAGTGGGCAT TGGGGGGAAG CAGAGCACCT GATGCTTTAC 150
TGCAGAAATN CCTATGTGAC TCTTATAA 178

35

(2) INFORMATION FOR SEQ ID :272:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCCGT ATGATGNGGN 100
NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150
TGCAGAAATN CCTATGTGAC TCTTATAA 178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGAAGAA GATCAGAACA 50
AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG 100
CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC 135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

151

(xi) SEQUENCE DESCRIPTION: SEQ ID :274:

50
5 CTTGTCACAN GAAAGCACCA TGTTGCAAT GGATTGCTGC AGGTGCTGCC 100
GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA 150
TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTTCC TTCAT 200
10 GACATAGGTG AGCAGTTTCC AGTCCCACTC C 231

(2) INFORMATION FOR SEQ ID :275:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25 TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC 50
TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA 100
GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG 150
30 NCGTNCCCAC CATTGATTGA 170

(2) INFORMATION FOR SEQ ID :276:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

152

(xi) SEQUENCE DESCRIPTION: SEQ ID :276:

	ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA	50
5	ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG	100
	AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC	150
	CTGAGGGAAA CTAATCTGGA TTCACTCCCT CTGGTTGATA CCCACTCAAA	200
10	AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA	250
	ACGAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT	300
15	AGCGTAGCAT ATTNA	315

(2) INFORMATION FOR SEQ ID :277:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 209 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :277:

	ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTTGAGA TTTCACAAGC	50
30	AATGCGAGTG TAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC	100
	ATAGTTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT	150
35	AGCAGAAATA GGCCCTTTCG TGNGCTGTTC TATTNCTCG GATNGTAGAT	200
	ATAGTAATC	209

(2) INFORMATION FOR SEQ ID :278:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

153

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :278:

10 AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC 50
TGCTGTAAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA 100
GAGTCTT 107

15

(2) INFORMATION FOR SEQ ID :279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :279:

ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA 50
CAGTGCAATA GGCTCCAAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT 100
30 ACTACTGCTT TAAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG 150
TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC 200
35 GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCNCT ATAAGTGCAC 250
AAAGGGGAAA CACTGATTTT AAGCTT 276

40

(2) INFORMATION FOR SEQ ID :280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs

154

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :280:

10	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
15	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT	185

(2) INFORMATION FOR SEQ ID :281:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 186 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :281:

30	AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
	CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
	TAAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA	150
35	GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA	186

(2) INFORMATION FOR SEQ ID :282:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

155

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTTCGAGA GTCCATGTTC 50
TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT 100
10 TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT 150
GTAGGCACAG GGAGACTCAA AAGCAGGAGT TNTGAAAGCG TAAATGGG 198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA 50
GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA 100
30 CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC 150
CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTTTG ACAGCTTTCT 200
35 CAGCTCCCTG ACTCCGTTTA CC 222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA 50

ATGTGNGACG AACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA 100

10

CCTTTGNCGC TGTTTNTGCA ACGTTCGCAG TGNTACTCTG CGTGAACCGG 150

TAGACTGCTT GG 162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC AAAGCCCACT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA 50

GACAGCAGAC TCGAGCC 67

30

(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

157

GGTCGGATCA GGTCAACCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA 50
GGCAGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT 100
5 TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA 150
GAA 153

(2) INFORMATION FOR SEQ ID :287:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20

TACTACGGCT AAGGAGAAAC AATGTTCTTA CATATCACGG GTAGTGAGAA 50
CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT 100
25 CCATCGTGCT TTAGAAATAA CTGTATACAG TGTTATAAGT TGAAAAGAAC 150
TCAAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG 200
CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC 250
30 GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC 293

(2) INFORMATION FOR SEQ ID :288:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

158

(xi) SEQUENCE DESCRIPTION: SEQ ID :288:

AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT 50
5 CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC 100
GTGTTGAATC ACTG 114

(2) INFORMATION FOR SEQ ID :289:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20

ATGAACCA GT GCGGAGGTA CCCGGGTGTG GACCAGAGAA GTTGCTGGA 50
AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC 100
25 CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC 150
GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC 200
AGCGTCCGGG AGCCTCCCTG TCCTTGTTG GGTATGGNG CTCTGGCGTT 250
30 GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT 290

(2) INFORMATION FOR SEQ ID :290:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

159

(xi) SEQUENCE DESCRIPTION: SEQ ID :290:

AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50
5 NACTTTGTTG CTTTGCTGAT TTTAACAGCT TGATTCTAAG CNCTTACTAG 100
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTTACTT TTGCTACTGT 150
TTTGTAGAAC GATGTACATG AATGAGCCT 179

10

(2) INFORMATION FOR SEQ ID :291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :291:

TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG 50
25 TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCTGT AACTCTGCTT 100
CTGTGGGATT CTGCCCAAGA GATTCATTA CAGTTCCCAA TTCTTTGTTG 150
TTATAGTACC ATCACCATTT CGTTAAATAG TGAAAGAGCT TTTTGAATC 199

30

(2) INFORMATION FOR SEQ ID :292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

5 GGAAGACCAT TCTGATCATC CTCACTGACG CCP GCGAA GAGGGTGGTT 50
TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT 100
CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC 150
AACCGAANNG ATATTACAAT GTAAAAA 177

(2) INFORMATION FOR SEQ ID :293:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20

ATTGGTTTTCTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA 50
CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC 100
25 AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT 150
TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAAC TTGN GTCTGTTTCT 200
TTTAGGCTCT TTTTGACGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC 250
30 CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GCGCT 295

(2) INFORMATION FOR SEQ ID :294:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

161

(xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG 50

5 CATATTTTAC CATTTTGNA AACTGTGAG 78

(2) INFORMATION FOR SEQ ID :295:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :295:

ATTCTGTACC TGTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATT 50

20 GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG 100

GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTGAGA 150

25 GAGCCCGGTA ATA 163

(2) INFORMATION FOR SEQ ID :296:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :296:

AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC 50

40 CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA 100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT 150
CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCCTC 189

5 (2) INFORMATION FOR SEQ ID :297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCTGTCCC CACTCACACA 50
AGTGGTCCGG TGTCACCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT 100
20 GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150
GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG 50
CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG 100
40 CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150

163

GTATCATCAT GCTGCCTCCT GCATTGAAT T

181

(2) INFORMATION FOR SEQ ID :299:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15 AACATTGTTT ATTCATCCAG CAGTGTGCT CAGCTCCTAC CTCTGTGCCA 50
GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTtagc ACAGCCTGGG 100
GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA 150
20 CTGCAAGCTG CTTGCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT 200
CATCTGGTTG TGA CTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT 250
25 TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC 300
GAGGCATGTA CATT 314

(2) INFORMATION FOR SEQ ID :300:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :300:

40

AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC 50

164

CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT 100
TTTAAGAACT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA 150
5 AAGGAGAGAC AAGTGCAA 168

(2) INFORMATION FOR SEQ ID :301:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :301:

ACCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG 50
20 GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG 100
CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT 142

25 (2) INFORMATION FOR SEQ ID :302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :302:

AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT 50
GATGACCAAC AAAGACTGAA GTTCCTATC TACGGAAAGG CATGACTGGG 100
40 AGGCCCCACAA GGACTCTCAT TGAGTTCTTA CTTGTTTCA GTCAAGACAA 150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG

197

(2) INFORMATION FOR SEQ ID :303:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15

AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT

50

GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC

100

CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA

150

20

TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT

200

AAAAGTTTTT GAATAAATGA TGAAAATTTT TTAAC

236

25

(2) INFORMATION FOR SEQ ID :304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :304:

ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC

50

CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG

100

40

TCTAGCACAG CCACCGCCCC CATGCCCAGG CTCAGGAGCA CACTGAGGTC

150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200

TTAGGCCTCC CGTACAAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA 50

ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAGNTC 100

20 AACCTTCGAT GCTATCCCCC AGCCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100

40 NGNTGATATA AACAGATNNA 120

(2) INFORMATION FOR SEQ ID :307:

167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50
TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNG 100
NGNTGATATA AACAGATNNA 120

15

(2) INFORMATION FOR SEQ ID :308:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :308:

30

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTATCAT 50
AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA 100
GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC 150
TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG 200
AGCCGGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG 247

35

(2) INFORMATION FOR SEQ ID :309:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

168

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG 50
AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT 100
ATGCCGTT 107

15 (2) INFORMATION FOR SEQ ID :310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG 50
ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG 100
TATCAGGAAA GAGA 114

(2) INFORMATION FOR SEQ ID :311:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

169

(xi) SEQUENCE DESCRIPTION: SEQ ID :311:

ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC 50
5 TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT 100
TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC 150
GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA 200
10 GTTGCATAA CCACCTCCGT AGCCCCCACC CTGTTGC 237

(2) INFORMATION FOR SEQ ID :312:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25 TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG 50
TGGTGACAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA 100
GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC 147
30

(2) INFORMATION FOR SEQ ID :313:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG 50
CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA 100
5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG 150
G 151

(2) INFORMATION FOR SEQ ID :314:
10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :314:
20

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC 50
AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA 100
25 AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT 150
TATCACTAGG CTAAAACCTGG ACAAAGACCG CAAAAGATC CTCGAACGGA 200
AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA 250
30 ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA 287

(2) INFORMATION FOR SEQ ID :315:
35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT 50
5 GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTTCCA 100
CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT 150
GTAAACTAAG GTAGACTACT CTGNGAATAA GAA 183

10

(2) INFORMATION FOR SEQ ID :316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :316:

GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTTCA AAAACGTGGG 50
25 TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100
CCACCTTTGC AGCCTGTTTC TGTGATGTAG TTTCA 135

(2) INFORMATION FOR SEQ ID :317:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :317:

40

CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC 50

172

TGCCGAAGTC CAAAAGCTTC AGCATTTTCCT TAGTGTGAGG ATCTACTTCA 100
ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC 150
5 CTATNTTTTC TGCGGCTTGA TGGAGATACC TTTACTG 187

(2) INFORMATION FOR SEQ ID :318:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :318:

TCCCAGGAGA AGGAACTTTG AAATTCATCC CAACGTAGGC TGAGTGACCT 50
20 GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTCAGCATT TCCTTAGTGT 100
CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA 150
25 ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT 200
GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN 250
AGCTTTCNGT TGNNTAA 268

30

(2) INFORMATION FOR SEQ ID :319:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGTA TGGAGATGTC ATTTATTATA 50
 AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA 100
 5 GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT 138

(2) INFORMATION FOR SEQ ID :320:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :320:

AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTC ATAAACCTCA 50
 20 GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT 100
 GTAATCATAC TTCCCCCA 118

25 (2) INFORMATION FOR SEQ ID :321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG 50
 GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC 100
 40 GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT 150

174

TTCCTTTTCC

160

(2) INFORMATION FOR SEQ ID :322:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :322:

15 AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCCG 50
AACAGGGCTG CTGATTGTTC CTTTCACTTT TGNGGTGACC TTGAGCTCCC 100
TTAAAAAAA AACTTGGAGA ATCACAACCTG GCAATGCACC GCAGTTCTCG 150
20 AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT 200
GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA 250
25 ACCCCCTGGG AGTATAATNN TCTCCATANA A 281

(2) INFORMATION FOR SEQ ID :323:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :323:

40 GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50
ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG 99

175

(2) INFORMATION FOR SEQ ID :324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50
ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA 100
CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA 150
TTGCCCCGCGT TTTTAGG 167

20

(2) INFORMATION FOR SEQ ID :325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAACCT CTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA 50
AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG 100
ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCCTCTT 150
TCGGGTCGCG 160

40

(2) INFORMATION FOR SEQ ID :326:

176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10

GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT 50
GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG 100
AACATGAGAG AGCAGAGTGC TCTC 124

15

(2) INFORMATION FOR SEQ ID :327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :327:

30

AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA 50
GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT 100
CGACAATGTA ACTCTGCAA TCGATGGAGT CCTTTACCTG CCATCATGGA 150
CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG 200
CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA 250
AGT 253

40

(2) INFORMATION FOR SEQ ID :328:

177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :328:

GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA 50
TAGAAGAAGC TCAGTATCGG CTCCTCCCAC CATAACCGCG TTNAATCGC 100
CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCATG CTCCTGCTAC 150
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTAT 200

(2) INFORMATION FOR SEQ ID :329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :329:

TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC 50
TCTTTCTTTT NTCGAAAATN ATAAACTGC GTATTCTACT TTATATTTAA 100
TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG 150
AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA 200
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA 250
GGATTACCAA CTCCTGCTG CCATGACCGA 280

178

(2) INFORMATION FOR SEQ ID :330:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CCTGAAAAAC TTTATGGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTTNT 50
15 CGAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA 100
AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT 150
TCATATGTTC ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC 200
20 AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT 250
CACTGCTGCC ATGACCGA 268

25

(2) INFORMATION FOR SEQ ID :331:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50
AGAGTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100
40 TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150

179

TACCATATGC CCTTAAAAAT

170

(2) INFORMATION FOR SEQ ID :332:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15 TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50
AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTGCATTN 100
TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150
20 TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGTTCTGT 200
GTTCCAAAAA TNTAAGATTT GTT 223

25 (2) INFORMATION FOR SEQ ID :333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAACCTCCA CAAGTTCTTC 50
TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG 100
40 TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC 132

180

(2) INFORMATION FOR SEQ ID :334:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC 50
15 TGAATAACC AGTGCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT 100
CCATNTTTC CAATTTCAAT TGTTTGGGAT TCTAGCACTC CTTACCNGCA 150
GTAATGCCCT TGCTGCAGAC AACACACCT GGACTGNGAG ATGGACCAAT 200
20 TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT 235

(2) INFORMATION FOR SEQ ID :335:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :335:

35 ATGCCCCGAC CATCCGCTAC CCGATCCCC TCATCAAGGT GAATGATACC 50
ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTCA TCAAGTTCTGA 100
CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG 150
40 GNGATCACCA ACAGGAGAG 169

181

(2) INFORMATION FOR SEQ ID :336:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCCGAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50
15 ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC TCAAGTTCGA 100
CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG 150
GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG 193

20

(2) INFORMATION FOR SEQ ID :337:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC 50
35 TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA 100
ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG 150
CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT 200
40 CATCTGCAGG ATTCCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCAA 250

182

AAAGGCAAAC TAAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG 300
CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CACAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50
CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTTAA 100
20 TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150
TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200
25 ATCTGCAGGA TTCCAGCTT TGCTCAGTCT TCATGCCCCAC CAGAGGCAAA 250
AAGGCAAAC TAAACTGTCA TGCAGTGGTA GGTTTGAAAT NAGCTGCTGC 300
ATCAT 305

30

(2) INFORMATION FOR SEQ ID :339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA 50
ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG 100
5 G 101

(2) INFORMATION FOR SEQ ID :340:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :340:

GTCGCAGGAG AAAAAAGTCG TCACGTCATG CGAGTGC GCA GGGGGCGTGG 50
20 AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA 100
AGGACTTCCC GCA 113

25 (2) INFORMATION FOR SEQ ID :341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :341:

ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAAAGCAAT 50
ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC 100
40 AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA 150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200

TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100

20 GCTTTTAATC TTCATTTTNN NNTTTTGTA TGGTAGGCTG AGATGCTTTT 150

AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200

25 TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250

TA 252

(2) INFORMATION FOR SEQ ID :343:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :343:

40

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100
GCTTTTAATC TTCATTTTTN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150
5 AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200
TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250
TACAAAAC 258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC 50
25 CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG 100
ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA 150
TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG 200
30 CACAGGACCC AGGAGTCCGC CCACCTG 227

(2) INFORMATION FOR SEQ ID :345:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50
5 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100
CTGGCACACT ACTAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT 150
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA 188

10

(2) INFORMATION FOR SEQ ID :346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :346:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50
25 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100
CTGGCACACT ACTAACTGT AAATGTTTTC AAATCTGAAT CTGTAGAATT 150
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT 200
30 NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC 250
TAGAAGTGNA AA 262

35

(2) INFORMATION FOR SEQ ID :347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

187

(xi) SEQUENCE DESCRIPTION: SEQ ID :347:

5	CTCTGTTTTC CAAACGCCCA TGTGTGCTAT ACTACAATC TTCTCGAGTC	50
	TGATCAATTT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC	100
	ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTTAAAAGA	150
10	AATNTCTAA	159

(2) INFORMATION FOR SEQ ID :348:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 283 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :348:

25	TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC	50
	ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT	100
	ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC	150
30	CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCCTC	200
	TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA	250
35	TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC	283

(2) INFORMATION FOR SEQ ID :349:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 169 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

188

(xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5	CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AAACNGTGG	50
	CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC	100
	GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG	150
10	TGGATCACCC AGGTCAGGA	169

(2) INFORMATION FOR SEQ ID :350:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 175 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25	GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC	50
	AACCCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT	100
	GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA	150
30	CTTGGCAACA NCACAGGAAG GGACC	175

(2) INFORMATION FOR SEQ ID :351:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 206 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

189

(xi) SEQUENCE DESCRIPTION: SEQ ID :351:

AAATAAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA 50
5 AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG 100
GCACACTACT AACTGTAAAT GTTTTAAAT TGAATCTGTA AAATTTGTAA 150
GGTTTATGA ATATAATATT ATTAATATT ATGTCTCTGA ATTTTNNNN 200
10 NAGGCT 206

(2) INFORMATION FOR SEQ ID :352:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25 AGACATACTG TAGTGTCTAA ATAATATTG TCNGAAGATA ACAATTATGG 50
GACTTTAAAG CCGACAGTGA AATTAT 76

(2) INFORMATION FOR SEQ ID :353:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40 ACATTGGGCC CTCAGACTGT AATTCCATA CTACTNTGAC TGATACTAGA 50

190

TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAAA 100

ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG 150

5 GGCACTGCGT TTAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC 200

GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA 245

(2) INFORMATION FOR SEQ ID :354:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20

GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC 50

AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG 100

25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT 150

CTTTGGGTTG AGACTTTTCA GNGACAACT 179

(2) INFORMATION FOR SEQ ID :355:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40

AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC 50

191

TCCAGCATGT TGTACCATT TCAACAGAAA TCGCACAAAT GCTACTGTGC 100

AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG 139

5 (2) INFORMATION FOR SEQ ID :356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAACTTC CACTTATAAC TGTNTCAGCC TGACTATAAT 50

GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT 100

20

(2) INFORMATION FOR SEQ ID :357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGA AACTAACCA 50

35 AGATTGGAC ATTGGAATGT TTAGTGTAT TCTTTAAGAA ACAACTACAA 100

AAAGAAAATG TCAACAAATT TTTCTAGCT AACTGAG 137

(2) INFORMATION FOR SEQ ID :358:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

192

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :358:

10	AAGGAACAAG TGGGTCATTC TCACTAAGGC TGCCTGTCAC TGCAGTCTTG	50
	ATCAGCTTGT CAATTTGATA CTTCAGCTTT TGGTCCAAGG GACGAAGCTT	100
	TTCCAAAACC GTTCGAATCT CTACCAGTCT CAAAAGTCA TCATGTCCCT	150
15	GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG	200
	GGNACATGAG CAGCAGCTGN TCTTTAAC	228

20

(2) INFORMATION FOR SEQ ID :359:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 248 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :359:

	CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT	50
	CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA	100
35	CACTCACCTT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA	150
	CCAAGAAAAT GAATAAAACA GCCAAACTCG ACCTTCTTAT GCAGAAAATT	200
40	GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC	248

(2) INFORMATION FOR SEQ ID :360:

193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :360:

10

AGGCACCTGT GGAGCCATCC TCCTTGTTTT AATCGTCCTG CTGCTGCTGC 50
CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC 100
TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA 150
CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT 200
GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT 250
GCC 253

20

(2) INFORMATION FOR SEQ ID :361:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :361:

35

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50
GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100
CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150
TAAT 154

40

194

(2) INFORMATION FOR SEQ ID :362:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50
15 GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100
CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTINGA TCGGTAGAGA 150
TAATCCTGNC CACGCCCT 168

20

(2) INFORMATION FOR SEQ ID :363:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA AGGAAGCTTT GNCACCACTC TACCATCAAA NNGGAATTGA 50
35 ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAAA CATGNATTTT 100
ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT 150
CTCTCTATTT NTTTCTCTGG TTGTCGACCA GCTGACTNTG NCATCGTT 198

40

(2) INFORMATION FOR SEQ ID :364:

195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGA AGGTCATAGT AAGCATACCT ATGCTGAGAG 50
AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC 100
TCGTACACTT TCAAGTTTAA A 121

15

(2) INFORMATION FOR SEQ ID :365:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :365:

30

GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA 50
AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAGAGTT TTCAATGCTT 100
TCTAAAAGTT TCCTCTTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC 150
GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT 200
CTCCAAGGGA G 211

35

(2) INFORMATION FOR SEQ ID :366:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

196

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

CGGCTACACC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT	50
GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC	100
ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA	150
AAGTTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG	200
ATACAGTGGC CTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT	250
TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG	285

20

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :367:

GAACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG	50
GTCTTGGCAG GCGAAGCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA	100
ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT	149

35

(2) INFORMATION FOR SEQ ID :368:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG 50
10 CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG 100
GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG 137

15 (2) INFORMATION FOR SEQ ID :369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :369:

GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTTATTTTT CTGTTAGTGA 50
CATGTAGTCC CTTTGTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA 100
30 TAGAGTAAAT ATTGTTTCCTT TGCCTACTCG TGCTTCCAAT GATTAAGGAA 150
ATGTTAAACA NNNGTNAAAG TCTGTTTTGT CAATGCGGGA GT 192

35 (2) INFORMATION FOR SEQ ID :370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

198

(xi) SEQUENCE DESCRIPTION: SEQ ID :370:

5 GAGACTTAAG TAAAACGGCT GCAGGCCAGA TTCGCCCACC AGCTCAGAGA 50
CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT 100
GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTCACGNAT 150
10 ATAGTAGAAA CCAAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAT 197

(2) INFORMATION FOR SEQ ID :371:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC 50
25 ATACACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC 100
GGGCTTTGGA GAGG 114

30 (2) INFORMATION FOR SEQ ID :372:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCTCCACA TTCCCTTCAG 50

199

CTCCTAGTTG TTCCACCTTG GCTAACAATT TACCAATCTT TTTTCTATG 100

AACACGTTCT GCCTTTGCTG CTA CTTC 127

5 (2) INFORMATION FOR SEQ ID :373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTTC 50

TTTTTCAGTT CTCCTGGTC TGTAACAGGA ATGCCCTTA CTCAGTAGCA 100

20 GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT 150

TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG 200

25 CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT 250

TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

200

NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT 100
CCGTGGGAAT CACTGTCTGA GTCTTGTC TAGTATTGAC AGATATAGCT 150
5 TTGTTCTTGG AGTAGAATTA AGGAATTGCG 180

(2) INFORMATION FOR SEQ ID :375:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :375:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50
20 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC 100
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150
25 TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAC ATCTTACTGA 200
TGCTTACTTC AAGAAGAAGA AGCTGCCGAA GCCCAGACAC CAGGAAGGTG 250
AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA 300
30 TTGATCAGAA AGCTGTGGAC TTA 323

(2) INFORMATION FOR SEQ ID :376:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

201

(xi) SEQUENCE DESCRIPTION: SEQ ID :376:

GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTTT CTAAGAGGTG 50
5 AAATCACTCG CTGGTGTTTA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT 100
ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTCACAG 150
ATGGGGGGTA GTTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG 200
10 AGTCAGTCCT GCATTTATGT CTT 223

(2) INFORMATION FOR SEQ ID :377:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25 GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTTCCC 50
CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTTGTCAT 100
ATGGCTAATC AAGAGCCAGG TA 122
30

(2) INFORMATION FOR SEQ ID :378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

GGCAGTGCCT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC 50
TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTCTC 100
5 AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA 150
AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT 195

(2) INFORMATION FOR SEQ ID :379:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :379:

20

GTAGCCCTGA GGTCACTCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG 50
GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAAGTTG GAAGGTTATA 100
25 GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN 150
GGTTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT 200
ATANNNNNGG 210

30

(2) INFORMATION FOR SEQ ID :380:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :380:

203

CTGGCTCACC TGGACAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT 50
GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA 100
5 ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA 150
CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG 200
GCCACAAGT ATCACTAAGC TCGCTTTCTT GCTGTTC 238

10

(2) INFORMATION FOR SEQ ID :381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :381:

GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA 50
25 ATAGCTGTTC ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT 100
CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAAC 150
GATTGGAAAT CTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA 200
30 AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAAACAGG TGGAAGAAAA 250
CCTAGCNCGC ACAGAACATA AGCTC 275

35

(2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5 AAGCAGAGTA CGCAGGTCAG GCCCTTCCAC GCCCAGCCCA AACTTTAAA 50
CNTACTGGGC GATGGGGCCG TTINGCTGGC AGTTCAAGAT AAAACA 96

(2) INFORMATION FOR SEQ ID :383:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20 GGAAGTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA 50
AGGAGCTCTG GGCACCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC 100
TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT 150
25 CAATNCNAAT NGANNGGTTA CTCAAAGGG ACGAGACATG CACCTG 196

(2) INFORMATION FOR SEQ ID :384:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
35

(xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40 AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC 50
ATTCAGCCT CACTTTGTGT AGGTCACCTT TCGGTCTGTG TTGTAGCTCA 100

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG 150
CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT 200
5 CCCCAT 206

(2) INFORMATION FOR SEQ ID :385:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :385:

GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTTAC 50
20 CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG 100
AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA 134

25 (2) INFORMATION FOR SEQ ID :386:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :386:

CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC 50
ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA 100
40 CCAGGACGCC ACGCCGACGA ACAAGGGGAG TTCNGAGGAG GAGGAGGCCA 150

206

GGACGAGGCG T

161

(2) INFORMATION FOR SEQ ID :387:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :387:

15 GGTGAGCCTC CGCCATCCAG CCAAAC TGTGC TGAC CGCAGCTGTG 50
CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGAACAC TGAAAACACA 100
ACCACTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGT 150
20 GTTTTTTNAG GCAGTAATNT 170

(2) INFORMATION FOR SEQ ID :388:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :388:

35 TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCTCTG 50
GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100
GCCCAATACA AAATACACAG AAAAAGCAAT TATTAAAAAC GGCTTCGGTT 150
40 TCTTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC 200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTC AACTGAAATC 250

(2) INFORMATION FOR SEQ ID :389:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15 GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCCTTCCT 50
CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT 100
CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN 150
20 TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG 200
AGACCNAACT TGCTCTAGCC CTTTCAGCC GCTGTTGTTA AACTGACCTC 250
25 GTAGGGCNTG AGGGAGGT 268

(2) INFORMATION FOR SEQ ID :390:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :390:

40 GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA 50
GAGGCGAGCT AGCCAGCCAA GCGGGGAGG CCGGGGAGGCC CTCTAGCTGT 100

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG 150

CCAGGTATAC ACCTTANAGA GGATGAC 177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA 50

TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG 100

20 GCAACCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAA 139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC 50

TATCTGGGGC GCCTGGCTCA CGAGGTGGC TGGAAGTACC AGGCAGTGAC 100

AGCCACCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA 150

40 AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCGGAG 200

209

AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCACGGA CTCCTGGTCT 250

GAGCCCAAT 259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGAAG GTACTGGTCC AATTTATCTA GGAAGTATCT 50

CTTGGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG 100

20 CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG 150

GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC 189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA 50

AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA 97

40

(2) INFORMATION FOR SEQ ID :395:

210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10

AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTT 50
GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC 100
CCCTTGACTG ATTTATTGTC GTCAAAAGCA TGTTCTCTA TCTTTTNNNN 150
TGGACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT 200
AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT 244

20

(2) INFORMATION FOR SEQ ID :396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT 50
TTTTATTCTG ATCTTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA 100
GCTTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA 150
TTGCAGCCTT TCTTTTCCGT TTCTTTTNTG AAGGG 185

40

(2) INFORMATION FOR SEQ ID :397:

211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :397:

10 GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG 50
CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG 100
15 AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC 150
ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTTGTCTGA 200
ACACTGCTTA TCTGACCC 218

(2) INFORMATION FOR SEQ ID :398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :398:

30 GGAAGCAAAA AAACAAACT AAGCTCGAAT TTGCTTCAA ACCTGTAGAT 50
35 TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC 100
CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAT 150
GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATT GACCCAGAA 200
40 AACCCAGTA CCTTTNNACA ATGACCCAAC CANTACCTAC CATCGGCCAG 250

212

(2) INFORMATION FOR SEQ ID :399:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :399:

TCACCTTGATT CATCCGTCGC GGGATTGGG AGCACTAGCA ACATAATCAA 50
15 CACACTCCTA CAATCTTAGG CTTACATGT GCTGATGATG ATGAAACCAA 100
CTCTGCCCCA ATCATCTCCC CTTCTNNTAG GGTCTTACTA CATATCGCAA 150
CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCAC TACCC 200
20 TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA 250
ATAATGAGAT TAAATTTATG TTTCCAGT 278

25 (2) INFORMATION FOR SEQ ID :400:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :400:

GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA 50
GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA 100
40 GCAAGCTCTC TTCCTTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTTA 150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA 200

ATGTGTT 207

5 (2) INFORMATION FOR SEQ ID :401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA 50

GGGGGCCAGC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC 100

20 AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC 150

AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG 200

25 NTTCTCCAAA GATAGCC 217

(2) INFORMATION FOR SEQ ID :402:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTTACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT 50

40 CTTCCACAC TCGCACATCG AAACATTTTT GTGCCAGGGC TTTCCAGCTC 100

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCCACATCT GGAACACTTC 150
TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTTTGG ATTTGTTGTA 200
5 GGCCTGTGAG GCTGAACACT CTCTG 225

(2) INFORMATION FOR SEQ ID :403:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG 50
20 ACTGNNGGCTT CCACTGCGCC CGTGTACNTT ATCGAAGCTA CAGAT 95

(2) INFORMATION FOR SEQ ID :404:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :404:

AGGAAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG 50
35 CAAATTCCAA AACAGAAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG 100
GGCCCACTG TGTAATACTG TGCCAACTTA TCGGAGTCTC ATTGTTTCAGG 150
40 ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATACC 200

215

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG

239

(2) INFORMATION FOR SEQ ID :405:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15 GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA 50
TGTTCCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG 100
AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA 150
20 GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC 189

(2) INFORMATION FOR SEQ ID :406:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35 CACCATCCTC CAAGTAAATC CCCCTTAGG AAAGTAAGGG AAAAGACCCC 50
TTATAGCCCT GAGCTCCCCC TTGGA 75

(2) INFORMATION FOR SEQ ID :407:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs

216

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :407:

10 TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT 50
TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT 100
CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG 150
15 CTGCCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC 190

(2) INFORMATION FOR SEQ ID :408:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :408:

30 GAAGACATGG CGCCCTAACA CTTCGAGACC TGCTGNTAAA TTTAAAGCTA 50
TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG 100
CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG 150
35 CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT 194

(2) INFORMATION FOR SEQ ID :409:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

217

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATT TAACCACTTC 50

TAAACAAGA TCATCTTCTG CAGCACCTGG TTTAGTTTA TCCTTGA 97

10

(2) INFORMATION FOR SEQ ID :410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTGAGCTCC TGGACCCTTC TTGCCTACA CTGGCCTTCC TCTCGGAGGG 50

25 ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNTTNTG GTCCAGGGCC 100

AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC 150

TTTGC 155

30

(2) INFORMATION FOR SEQ ID :411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA 50
AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC 100
5 TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG 150
TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA 200
TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT 249
10

(2) INFORMATION FOR SEQ ID :412:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCAGC 50
25 TTTACTCCTC TATAACTCAT CTTACACCN GCATATTTAA ACAAACTAAC 100
AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT 143

(2) INFORMATION FOR SEQ ID :413:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCC ATTCACGTAC TCCATCACA AGTACAGGCG GTCCATGGTC 50

219

TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGCCTTCCCG GGCAGGCCAA 100
CACCCACTTC TCCACCATAG TGCACTCCAC GTCATCATCT GATCACAACG 150
5 TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT 200
GAAAGCATGA CTTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT 250
AAAATC 256

10

(2) INFORMATION FOR SEQ ID :414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :414:

TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA 50
25 GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC 87

(2) INFORMATION FOR SEQ ID :415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :415:

AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT 50
40 TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCGCCCGC 100

220

GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC 150
ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG 200
5 CAGTGTTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC 247

(2) INFORMATION FOR SEQ ID :416:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 162 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :416:

TCTAGCACAC AGCTGCGCTC ACAAAAACCTG CGCGACTTGT TAGAACTAAT 50
20 TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGCCTGCAGG TCAGGTAAGA 100
TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATT 150
25 ACATTGAAAG GA 162

(2) INFORMATION FOR SEQ ID :417:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :417:

CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTGGGGC TTATTTTAA 50
40 GTACTTAGCA AAATATTTGT TTNCGTGAT TTAGCTTGTC ATTAAACNAA 100

221

GAGCTACTG

109

(2) INFORMATION FOR SEQ ID :418:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15 GGATGTAAAT TATATGTTGT TTAAATTTT CCAGCATCTG AAAACCTTAT 50
CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTTT 100
TAAATAGTAC ATATCATTAA ACCATT CNTT CTAAANGTAA GAAGAGCAGA 150
20 AAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA 200
AA 202

25 (2) INFORMATION FOR SEQ ID :419:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC 50
ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACAG 100
40 CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC 150

222

TA

152

(2) INFORMATION FOR SEQ ID :420:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15 CAGCCCTACA CTCGCCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA 50
TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA 100
AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTGG 150
20 CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT 200
CTGCAATGTA GGGGCCGG 218

25 (2) INFORMATION FOR SEQ ID :421:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAACT CCCCCACCCA 50
GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC 100
40 CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC 150

223

TGCTGGCTGT CCTATGCCAG CCTCAGCAT GTGGGGACCA CGNAAGGCAC 200

ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA 237

5 (2) INFORMATION FOR SEQ ID :422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGGNGTAATA AATACTGCAT CCTTCCACA ACATAGCAGG AATCTTATAG 50

GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG 100

20 TTTCTTTACG AAGTGTAAT AAGTGCTGCA CCATACTGTA AACAAAACCTC 150

GAATATTGAC TAAATAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT 200

25 CC 202

(2) INFORMATION FOR SEQ ID :423:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG 50

40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA 100

224

150 TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAT
200 ACTGACTTCG GTTCTTTTT CTCTTCAAT NCCTATAATN GCTTTACATA
5 216 TTCGTATCAG CACCTA

(2) INFORMATION FOR SEQ ID :424:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :424:

20 50 CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT
100 GCTCGCTGGT CTA CTGCCAA AACCCATTTC ACCAACCATA TGTCCCTCGC
150 CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG
25 168 GGTGCCCTTT TAAAAAAA

(2) INFORMATION FOR SEQ ID :425:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :425:

40 50 TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGTTAC
100 TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA

225

GAGGAGTCAC AGTGGAAGTT CCCAGCTTTA AGATATCTAG CAGAAACTAT 150
AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG 200
5 GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC 250
TAATTAGG 258

(2) INFORMATION FOR SEQ ID :426:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20

TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG 50
CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN 100
25 GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC 150
CATGCACGAA GGACTTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCACG 200
CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTGTGCC AGCTGCTGTT 250
30 CGAATNNTTT TCTTTCTCGT AAAGC 275

(2) INFORMATION FOR SEQ ID :427:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

226

(xi) SEQUENCE DESCRIPTION: SEQ ID :427:

CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA 50
5 GAAGCCGAGA GGCAAAATGT CATCATATGC ATTTNTGGC AAAGTGTGG 100
GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT 150
CTAAGAGTGC TC 162

10

(2) INFORMATION FOR SEQ ID :428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :428:

ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC 50
25 CCATAGTTCC TGAATCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC 100
TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA 150
GTCGNGTTTA CAATGATTG NCCTGGACTG AAATTCANGC TGCCTTAAGG 200
30 TGCTGATGAT ATTGAGAAGT 220

(2) INFORMATION FOR SEQ ID :429:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA 50
5 GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT 100
GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG 150
GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA 185

10

(2) INFORMATION FOR SEQ ID :430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 277 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :430:

GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC 50
25 TACCTGGTCG TGGGAGTAGT GGTGATCGTG GACCCAGGGG TGATCCCTAT 100
CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC 150
TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG 200
30 GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG 250
GAAGACACCG CAGAGCTCAC TTACCAA 277

35

(2) INFORMATION FOR SEQ ID :431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

228

(xi) SEQUENCE DESCRIPTION: SEQ ID :431:

5 AAAGTGCCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGCCTGGTC 50
GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT 100
CAGCAAGGAG GAAGAAGTCA TTGTT 125

10 (2) INFORMATION FOR SEQ ID :432:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT 50
TCGAAATAGC ACATTTTTCAG CAATAGGCTC TCTACACTAG AGAGCCAGTA 100
25 GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150
AATCCCCC TTTATAAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200
30 ANAANGGAAA TGGGGCAGGA CA 222

(2) INFORMATION FOR SEQ ID :433:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :433:

229

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50
CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100
5 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150
TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200
NGNCGTTTCC TCT 213

10

(2) INFORMATION FOR SEQ ID :434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :434:

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50
25 CGATTTCCTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100
CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150
TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200
30 NGNCGTTTCC TCTGCCGGTG T 221

(2) INFORMATION FOR SEQ ID :435:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT 50
5 TAGTATATTT TCGTTGTCAG 70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT 50
20 CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA 100
GACTGATTGA GTACAAAATG AAAGTGTGCG TCAGCTTGAT CCATTTTGTC 150
25 ACCCTCAAGT AGG 163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA 50
40 AGAAGAAACA GAGGACAAAA AAACAGACGT TAAGGAAGAA GATAAATCCA 100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150

CTCAGCAACC CCTGAATTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50

AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100

20 GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAAGTGTGT 150

AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTTCGAGA AACAATAGTG TATGTGTTCC TATAGGTATG 50

AGTTATTCAN TGTAGATTG TTTTCTGCA ATCCTCTGCC GAAATGATNT 100

40 ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA 200

CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTCAG CTTTCCAGTT GACACCAAGT 50

CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA 100

20 CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200

25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50

40 TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

233

ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT 150
GGAATAGGCT TATTAAGTTA CACATTAAA AAGTCATTAG AACATCTCGT 200
5 TCTTGACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT 250
GGTT 254

(2) INFORMATION FOR SEQ ID :442:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50
CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100
25 CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC 147

(2) INFORMATION FOR SEQ ID :443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :443:

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50
40 CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100

234

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC 150
TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT 198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTTCCCTACA TATTATGGGT AGTGAGACAT 50
TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTCA 100
20 TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA 150
ATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT 200
25 TTCTGTGA 208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTTC ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT 50
40 CACTCTTCTC TCCAGCTTGG CCATTCTCTA TTCCTTGCGG GCCTGCCCTG 100

235

TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCTGTAA 150
CCTGNAGCCC CCGCTGAG 168

5 (2) INFORMATION FOR SEQ ID :446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCCTGATT GGTGGATAAA 50
GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA 100
20 TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA 150
AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA 200
25 CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA 243

(2) INFORMATION FOR SEQ ID :447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAAT GATTGCCAC CTGTTTTAGA 50
40 AATCTAAAAT NNTAAGTAAC TAAGAGCAAA GTGCTATGTG GGTTTTAGAC 100

236

CATGACTGTT TGTTTGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG 150
CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GGTGCTCTGG 200
5 GGAGGAGAGA GGAGAGAACA GGCTGTTTTG GAAAATATCC AGCACTTTGA 250
C 251

(2) INFORMATION FOR SEQ ID :448:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20

ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNGCAGGA ACGTGATGGC 50
AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAACATAT 100
25 ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAATAA GTTTTTAGAT 150
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA 200
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA 250
30 GTG 253

(2) INFORMATION FOR SEQ ID :449:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA 50
5 ATACCTCTGT AAGAAGCAGA ATACACCATA TGTATTTCAC ATGTATAGGA 100
GTGATAAGAA AAT 113

(2) INFORMATION FOR SEQ ID :450:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

20

TAGCATCCAG GGGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA 50
GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA 100
25 AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG 150
AAACTATTTG AGATCAAAGT CCTATAACA AAGTTAAATG ATTCCAAGAG 200
GTAAATAGGA G 211

30

(2) INFORMATION FOR SEQ ID :451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

238

CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG 50
NATTTACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTNCTG 100
5 TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTCAAGCA 150
GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG 194

(2) INFORMATION FOR SEQ ID :452:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA 50
TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT 100
25 TAAAACTACT TGAATTTCTA CTTCATAATA GGAGTCAGTC ACTTCTGGGA 150
CTATAGTGAT GCTTGCAA 168

(2) INFORMATION FOR SEQ ID :453:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCCAGAC GTGAACCAAT 50

239

TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCTTCAC 100
TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA 150
5 TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA 200
TAGGACGCCA GACTACACTG 220

(2) INFORMATION FOR SEQ ID :454:

10

(1) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20

GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA 50
AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT 100
25 TGCTTTTGAG TTCCTCAGCG TCTCTGAATN TTATTGGTTG GACATTCCAT 150
ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTTCAA 200
ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA 250
30 TAGTTTTGCT TTGTCTTTAG CGGTT 275

(2) INFORMATION FOR SEQ ID :455:

35

(1) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

240

(xi) SEQUENCE DESCRIPTION: SEQ ID :455:

TCGCAGAAGG AGGAACGGGG ACTTTCCATC CCCTGAACCA AGGCATGTTA 50
5 ACACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG 100
CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGACTIONCTT 150
AACANNTATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGGA ATCCATTTTG 200
10 TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA 250
TGCTCTNGGG TCTGCCCCATT 270

15 (2) INFORMATION FOR SEQ ID :456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCTCACT TAGATGATGC 50
ACGACCCCTG CGCTGGATAC GGCACGGTT TCTCATTTG CCTTTGCCAG 100
30 CTCTCATTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT 150
TTCTTAAGGA GCAAAACAGC TTCCTTGNNC TTCTTGTAGC CTTCAACTTA 200
35 TTAAACTAC CAAGGAAGTT CAGGAAGTTC CTCAANACGA TGACCTTTAG 250
ACAT 254

(2) INFORMATION FOR SEQ ID :457:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

241

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

ACACTAACTG TTCCATCCGT TATATTGCT GTGAGGAAAA TTAAGATTCC	50
10 TGTGTATGG GCTGCACTGT TTCTGGAAGA CTACAGAAAA TCTAACATGG	100
TTGACACTTC CTGGTAGCCC TTCTGTACAT ACACACACAC AACCAAGAGA	150
15 GAAGACAGAG AGAAAATCCT GGTCCAAAAG ATCACATGAC CTTACTAGTG	200
TTTCCCAAT GACTGTAATT TATAAACTAA AAATTG	236

(2) INFORMATION FOR SEQ ID :458:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

30

GAGANNNTT NNGGNAATG NTTNCGCACT GNAGCTAAGA ANAGNNATGG	50
NNNTAGGGNG NNAGANGNCN TGAACAGAGA AAGCNTGAGG GCTCTGGGAC	100
35 GCTGGTAT	108

(2) INFORMATION FOR SEQ ID :459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

242

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC 50
CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC 100
CCATGTTTCCT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA 150
GAGGT 155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC 50
CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT 100
CTGGTTTGTG GAGGTTTACA GACATGTGTT AGTATATCCT TGCCTGCATG 150
TAGTTGTTCA TTACTAGAC 169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

243

(xi) SEQUENCE DESCRIPTION: SEQ ID :461:

5 ACCNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT 50
CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT 100
TTTATCAGCG TACCTTTTTT GCCATGCGCT ACCTGCTATT GATGAAGGCG 150
10 GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT 184

(2) INFORMATION FOR SEQ ID :462:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :462:

25 AGGAACCN TG TTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT 50
TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA 100
GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA 150
30 GGCGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN 200
AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTCGGCCGT 250
NNACTGNGTT GTTGGCGACA GATGT 275

35

(2) INFORMATION FOR SEQ ID :463:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

244

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5 AATCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA 50
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT 100
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA 149

10

(2) INFORMATION FOR SEQ ID :464:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :464:

ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT 50
25 CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT 100
GTTCTCCTCG TCCATCAGAT CTCATAGGCT CAGAGACTGC AAGCTGCTTG 150
CCCAAGTCAC ACAGCTACTG AAGACCAGA 179

30

(2) INFORMATION FOR SEQ ID :465:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :465:

245

CTACCTCTGT GCCAGGGCAG CATTTCATA TCCAAGATCA ATTCCCTCTC 50
TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA 100
5 GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA 150
CCAGAG 156

(2) INFORMATION FOR SEQ ID :466:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA 50
CTGCTGGTTC TGTTTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC 100
25 TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGGCCTCACC 150
ACTCCCCTNT GTCCCCCAG CAGGGGGACA AAACAG 186

(2) INFORMATION FOR SEQ ID :467:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

TNNNGATGAN TATANAAGCA TCATNGACGG TATTTCCCG TCTTGNANTT 50

246

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

(2) INFORMATION FOR SEQ ID :468:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15

ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA

50

TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTTGCCTGG TATTGTGTTG

100

AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT

150

20

AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA

187

(2) INFORMATION FOR SEQ ID :469:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35

AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA

50

GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT

100

GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA

150

40

ACATCGGCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA

200

247

GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA 250

ACTGAA 256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT 50

GAAGTCTGAA TGGAGCCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA 100

20 GAGGGTTTG 109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAACTTT ATCAATCATA 50

GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTTGC TTGNAGACCT 100

ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTTCT 139

40

(2) INFORMATION FOR SEQ ID :472:

248

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10 TCGCAGGAGA AGGAATGTTT CCAATAGGAA CGCCTGTAGA CTGTTAGAA 50
 GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG 100
 15 GCTCTGAGGA CTATAGATTT ATCCTCTAGG TGATGAGGGA CTATTAACGG 150
 CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTCACGT 200
 GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA 250
 20 TGGGAGACAT TT 262

(2) INFORMATION FOR SEQ ID :473:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30

(xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35 ACAGAAGGAC TTTGTCTCTT TAGCTTGTTC AGCTCAATGA ACATTATCTC 50
 GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT 100
 GCATCTCTCA TACTTNNATC AGCCAACATC AACACTCTAT GTATTTTCTA 150
 40 AGCTTTCNTC TGTTCAGAA CTTTGAATTT AAAACGTCT 189

249

(2) INFORMATION FOR SEQ ID :474:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACCTAA ACTCGAACGC ACGTAATAGT GCTCATAATT 50
15 CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGACTCTAGC 100
AGCCTCGCTA ACCTAGTTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT 150
GTTAGTACGC GNGTTA 166

20

(2) INFORMATION FOR SEQ ID :475:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT 50
35 TCCTTCAAAA CTGTGTTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT 100
TCAACTTAA 109

(2) INFORMATION FOR SEQ ID :476:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

250

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :476:

10 TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA 50
GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA 100
CGGGTCACTC AGTTACGTTT AGCCACAGCC T 131

15

(2) INFORMATION FOR SEQ ID :477:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :477:

ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCTTAC 50
ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100
30 TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC 150
AGTGTTATAA GTTGAAAAGA ACTCAAATA ACTAATACAA ATATACACTA 200
35 CGTATTAGAA TTCAAAAAG CTGCTTCTG TGAAGTCAAT CAGCTATATT 250
AAAAAAGACA CAAAT 265

40

(2) INFORMATION FOR SEQ ID :478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

251

(B) TYPE: nucleic acid
(C) STRANDEDNESS: doubl
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :478:

10 AATCTACCAA CCTTAAAGCT CCCNGATAA AGCTGTATTT CCAAAGACC 50
TGTNTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTGT 100
ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT 150
15 NTTTCATCATG GTGTTGTCTA GGTCTCCTGA GG 182

(2) INFORMATION FOR SEQ ID :479:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :479:

30 AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAACCA 50
CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA 100
AACGGGAGCC TCTAAATCTT GGTGGGACT GCTCGCCTGG AGCCGCACTC 150
35 TTGAGTCCGA GGCCATCTT 169

(2) INFORMATION FOR SEQ ID :480:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

252

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTNENCAGT 50
CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTCTGTGTC TCACCGGATA 100
10 TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCT 150
GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA 200
15 ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC 238

(2) INFORMATION FOR SEQ ID :481:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC 50
30 TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCGAA GTCTGCAAGC 100
AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG 150
35 ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCTGT CTGAGGGAGG 200
C 201

(2) INFORMATION FOR SEQ ID :482:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

253

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

	CGGCTCAGNC TGTTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
10	CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
	CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
15	ACNTTTTTAG AT	162

(2) INFORMATION FOR SEQ ID :483:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

	ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
30	ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
	AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACNT NCCTGAACCT	150
35	GAGGGAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
	CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAACT	250

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 base pairs

254

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

10 AACATTATCT TGACAACTG AAGAACAATT CAGTTAACAC TACCTCGAAG 50
AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG 100
ATTAGAATGT TAATGCCACT TTGATTAGAT CT 132

15 (2) INFORMATION FOR SEQ ID :485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :485:

TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC 50
CGCATTACAG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC 100
30 ACGGACTTCT CGACACCATC AAGAGCGAC 129

(2) INFORMATION FOR SEQ ID :486:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

255

(xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG 50
5 AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG 100
ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTGT 150
CATTGCACTT CAACCATATC GA 172

10

(2) INFORMATION FOR SEQ ID :487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAAACTAAAT GGATCCATTA AAAGTTATGA 50
25 TTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA 100
TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC 150
AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC 200
30 TCAGATATAT 210

(2) INFORMATION FOR SEQ ID :488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50
5 ANACGCTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA 50
20 TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG 50
CCCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC 100
TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150
40 GCTTCGGAGA TGCAGCATCT GCGGCCAATG CCCCCG 186

257

(2) INFORMATION FOR SEQ ID :491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :491:

AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA 50
ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT 100
TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT 150
GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG 200
CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC 250
TTCATATCGG AAA 263

(2) INFORMATION FOR SEQ ID :492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :492:

AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT 50
AAATNGGTGT GGGNGGTCCG CTTTGGCCA TCATCGCACC CCCCCGGTCA 100
CTGGGCGTTG TTGCCGGGCA CTGTTTNNC NGGCTGGGTG TGTACCGTAA 150

258

CCGTGGGTC

159

(2) INFORMATION FOR SEQ ID :493:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15 GGGCAGAGNA AGAACTGTTT CACCAGGTGA ACAGTCCTAC CTGCTTGGTA 50
CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT 100
CAAATCAAGG TATCGGGAAG AATAATTTCC CCTCGATTCC ACAGGAGGGA 150
20 AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT 197

(2) INFORMATION FOR SEQ ID :494:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35 GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA 50
GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC 100
CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG 150
40 GGAGGGCTGC TGTGAGTGA GTCTTGAGTN GGTGAGTG 188

259

(2) INFORMATION FOR SEQ ID :495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCG 50
GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTGCCACG AGAGTGAGAC 100
GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT 150
GTGGGNGCTG CTGGGGAGG 169

20

(2) INFORMATION FOR SEQ ID :496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTCTATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG 50
AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGGAAGTCCC 100
ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC 150
TTTAAACCGT CAAGCTGGGT GG 172

40

(2) INFORMATION FOR SEQ ID :497:

260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :497:

10

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCCTCCAG 50
TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCCGGTC 100
ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA 150
ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCACCCC TTAGGGTGTG 200
TNTCATCGAA GTGTAGNGAA TGGTGGAAAG TTTGTTTGTN GTGTGC 246

20

(2) INFORMATION FOR SEQ ID :498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :498:

CCCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT 50
CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG 100
CCACTATTTT TGTTGTATAT CTTCATCTCA ATGGCGACAT GGCCACTGCC 150
CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT 200
GAACATCGTG CGTTA 215

40

261

(2) INFORMATION FOR SEQ ID :499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT 50
AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCTGTTCC 100
ACANGAAAAT AAAGCTAGGG AGGTGATTTA TCTATCCGAG AAAAAAGCCG 150
GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT 195

20

(2) INFORMATION FOR SEQ ID :500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT 50
GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAAATG CTTCAACAA 100
ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTAAAG GTGCACAAAG 150
TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG 200
CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG 250

40

262

GTGGAGCTGT

260

(2) INFORMATION FOR SEQ ID :501:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15 AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT 50
TAAATNCGTT GCTACAAAGT GTTTTGTTC TCTAAAAAGT AGTTTTTGCA 100
TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTGCT TTATATACAA 150
20 CAGTTAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA 200
CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA 250
25 ACCATGGCTT GCCCAAAT 268

(2) INFORMATION FOR SEQ ID :502:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :502:

40 AAAAACTCTA ATCCAGACTA CAGTTGTGCA GATTCAAGTC GTGAGTGCAG 50
GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC 100

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA 150

CC 152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC 50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA 100

20 NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T 141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC 50

GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG 100

GCCGAGC 107

40 (2) INFORMATION FOR SEQ ID :505:

264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10

ACCCTCTTCT GATAAATTG AGGGCCCGTT TGTCTTGGA GACCTTCAGT 50
AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT 100
GTCCCGCACG AACTTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG 150
CTGGGCTTGC TCACGTTCTT GTCACTTTGT GGCCCTTGTT GAG 193

15

(2) INFORMATION FOR SEQ ID :506:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30

ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTCCTACA 50
TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100
TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT 150
GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT 200
TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250
TGACACAAAT CCAAACAAGA TGCA 274

40

265

(2) INFORMATION FOR SEQ ID :507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :507:

CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA 50
AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA 100
GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA 150
AGTGTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AACCTTCAA 200
CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA 250
CCATTGAGAA GATGCAGGAG TAAAGTATTA T 281

(2) INFORMATION FOR SEQ ID :508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :508:

AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG 50
CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA 100
GCAGAGGGGA CAGAGATGAT GACCCTTTCG CTCCCCCTG CAAATGAGCC 150

266

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

180

(2) INFORMATION FOR SEQ ID :509:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

15 AAATGCAAAA CTCACCGTGC ACACTCCTAG ATCCCTGCCA CAAAGAAATC 50
TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT 100
ATT 104

20

(2) INFORMATION FOR SEQ ID :510:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG 50
35 GGAAGCTAGA GCCAGAATCA GGAAATCTG TTTCCTCGTC CCCAGACTCC 100
CGCCAAGCCT ACTCCACTAA CTACANNGA CTCTATCAAG TTTCTATCAA 150
GACTTGCAAT TGNATCTTGN A 171

40

(2) INFORMATION FOR SEQ ID :511:

267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10 ACTGTACCTA TCATCCTGAA AAACCTTTATG GGGGAGAAAG GTCAGCAGCT 50
TCTCTTTCTT TTNATCGAAA ATAATAAAAC TGGGTATTCT ACTTTAACTA 100
15 AATGTAAGGA AGAAAATATA CAAGCCCAT A TTTAATGTAT TTCTATNCGA 150
GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT 200
GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG 250
20 GATTA 255

(2) INFORMATION FOR SEQ ID :512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :512:

35 GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT 50
TTCTTGCTTT ATTTGTGACA TTTCAGTTTA TTAGAAATCA TGTTACCATT 100
AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTGATTT GTGTAACCTG 150
40 ATAAAAGATT TACTGACTTA AGCTTTTGTT TTTTTCATA AGCTGCTTTT 200

268

GAGCTTTGTC

210

(2) INFORMATION FOR SEQ ID :513:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15 CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA 50
AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG 100
AACAGGGATT CTTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAAA 150
20 AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG 200
AAGAAACAAA CGTGTGCATC CT 222

25 (2) INFORMATION FOR SEQ ID :514:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT 50
GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC 100
40 AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA 150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACCTCT TAAACCTCAT AGCNAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAATA ATCTAANGTA 50

ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA 100

20 TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATAACACG 100

40 AACACTCATA CACACANGCT TGTGCACACA TGTTATGCA CATGCATGCA 150

270

CTCACACTCA TACAAACGCA CATTTAAACA CGTGTGNACA NTGTACTCAG 200

ACACACACAG GTGTG 215

5 (2) INFORMATION FOR SEQ ID :517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA 50

GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG 100

20 TGTCGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC 150

AATCATGGGC CCTAGCCGNC CTNGTAATAC G 181

25 (2) INFORMATION FOR SEQ ID :518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTA ACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT 50

GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT 100

40 AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA 150

271

AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT 200
CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA 250
5 CCTGGCAACT 260

(2) INFORMATION FOR SEQ ID :519:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :519:

AAGCTAATAC AATGGTCATT TCCAGACAAA TTAAAGGAA AACTAAGGC 50
20 TGCTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA 100
CATGCTCTTT TTTA 115

25 (2) INFORMATION FOR SEQ ID :520:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :520:

CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTCGCAGA 50
AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA 100
40 CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT 150

272

GACTNATAGN TNGACCCACC TGTGA

175

(2) INFORMATION FOR SEQ ID :521:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15 ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT 50
TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100
20 TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTTCA 136

(2) INFORMATION FOR SEQ ID :522:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :522:

AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG 50
35 GATATATTTT GTGTCTTCTG TGACTGTTCA TTCATGGAAG GAAGCAGACT 100
GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC 150
TATTCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC 200

(2) INFORMATION FOR SEQ ID :523:

273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :523:

10

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT 50
CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA 100
CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC 150
ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA 200
CATA 204

20

(2) INFORMATION FOR SEQ ID :524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT 50
GGCAACAAGT GCAGGTTTTT TGGCTTTCTT TGATTCATAT TGTGCAAGAC 100
GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA 150
GAGGTCAATG TATCATCA 168

40

(2) INFORMATION FOR SEQ ID :525:

274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :525:

10

AAACTGTTCT TTAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT 50
AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTG TCCTTTCTCA 100
GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC 150
ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAACTGT 200
TTATCTCCCT CTGCATTCAG ACCAGGCTCC TTAGTGCACT CATCAGACTA 250
TCGCTGCCCC TGCTGTCTGC TGTGAGCCT TCACCACCAC T 291

20

(2) INFORMATION FOR SEQ ID :526:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :526:

35

CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAACCTCA 50
TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC 100
CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG 150
AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT 200

40

275

GGGAAGC

207

(2) INFORMATION FOR SEQ ID :527:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15 AGCATTCCGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC 50
AGGTCTAGGG AGGTTGTTC A GGAGCTCATT GATGAGTACC ATGCGGCCAC 100
CCAGCCAGAC TACATTCCT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC 150
20 CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC 200
CTCTGACCCA GCTTCACC 218

25 (2) INFORMATION FOR SEQ ID :528:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

AACCTNATGA CTCTCCATCC CCTTGAACCA AACATCTAGC ACTCAGCTCC 50
AGCATATTTT ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT 100
40 GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC 150

276

CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT 200

TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGCA 50

ACAAGTGCAG GTTTTGTCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100

20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50

GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT 100

AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA 150

40 TATGCACATG CTGGTGCTAC CCTCTCACT 179

277

(2) INFORMATION FOR SEQ ID :531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAT ATCTTCTCAG 50
CATTCAAAAC AAAACGCATA AGTCATTCCCT AACTNAGAG CTTTATAGCA 100
TTTTCTAGA CAGGAAGGGA AAAACAGTT AGCATTTAAA AGTCCGGAAA 150
GCTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTTG TCCAAATCCC 200
TTAT 204

(2) INFORMATION FOR SEQ ID :532:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :532:

AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC 50
CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC 100
CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTTAAATACC 150
CTTTCTTCAA AACTTAGCTC TGAATGGAGA AAC 183

278

(2) INFORMATION FOR SEQ ID :533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :533:

GAAACAAGTT CTCGCTCATC CCTGCATTTT TGCCAACTTC AGCTTGCAAT 50
ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC 100
TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG 150
TTTCACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG 200
GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT 250
AGGAGGAATA ATTTTCTCCT TCTNTGTAT CGNCTCT 287

20

25

(2) INFORMATION FOR SEQ ID :534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :534:

AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT 50
GACTTTTTGC AGTCAGTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG 100
GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT 150

40

279

TTAG

154

(2) INFORMATION FOR SEQ ID :535:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15 GATTACCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG 50
GGCCTATTTC TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA 100
TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG 150
20 GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC 200
CTAGGAAGGC AC 212

25 (2) INFORMATION FOR SEQ ID :536:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACG GATCATTTTT 50
ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC 100
40 CTGCCCCCTG GGAAGGNACA GTGATGTCTT TAGGGGAAGG AGGAGCCCCCT 150

280

NTCGGCAGTT GTCTTACT

168

(2) INFORMATION FOR SEQ ID :537:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15

CGGATCATTT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT

50

GTTCCCTGCT GCCTGCCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGGAA

100

GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNTAA TGAAGTA

147

20

(2) INFORMATION FOR SEQ ID :538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :538:

GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG

50

35

GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT

100

GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT

150

GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA

200

40

AATNAATGTA AACCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC

250

281

(2) INFORMATION FOR SEQ ID :539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :539:

AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT 50
GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTCGGGG ATGGTGAATG 100
CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC 150
CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGCC 184

20

(2) INFORMATION FOR SEQ ID :540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :540:

AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA 50
CCAGGGAAGT CACCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT 100
CATCATCATG TCTCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC 150
AGAT 154

40

(2) INFORMATION FOR SEQ ID :541:

282

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA 50

ATTTTGTTTT CTTCGTGTT ATTGGTTCAA AGTACTGGCC TTTCCTTCA 100

15

TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA 150

TGATTGGTT ATACTGTGAA ACAGC 175

(2) INFORMATION FOR SEQ ID :542:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT 50

CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC 100

35

AGCCGTGCTG CTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT 150

GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG 200

AATCGCGACT GGCNAACAGA T 221

40

(2) INFORMATION FOR SEQ ID :543:

283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :543:

10

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG 50
GAGAAACATA CCTTGAGAGG GGGTTTTCTT TAAACTAGT GTTAGAAGCT 100
TAGGGATTTT TTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA 150
TTTGACTTGT GCCGACATTG CAACTTTNT GACAGG 186

15

(2) INFORMATION FOR SEQ ID :544:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :544:

30

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTCTGCCT 50
TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA 100
CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT 150
GCC 153

35

(2) INFORMATION FOR SEQ ID :545:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs

284

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :545:

	GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG	50
10	TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT	100
	ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG	150
15	CCCAGGCCTG T	161

(2) INFORMATION FOR SEQ ID :546:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 188 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :546:

	AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA	50
30	GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAAC TGGGAAGGTCA	100
	TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA	150
35	TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA	188

(2) INFORMATION FOR SEQ ID :547:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 218 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTCTG 50
ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA 100
10 GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT 150
TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG 200
15 AATCACTCAT TTAGAAAA 218

(2) INFORMATION FOR SEQ ID :548:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT 46
30

(2) INFORMATION FOR SEQ ID :549:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG 50

TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG 100

5 AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTTCNC 146

(2) INFORMATION FOR SEQ ID :550:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :550:

AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA 50

20

ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT 100

TGACTCTAGT CACCTTGTTG TGCAGCAAG TACTAGGTCT TATTCATTCT 150

25

TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA 200

TTTTAAAAG ACAATGCTAG G 221

(2) INFORMATION FOR SEQ ID :551:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :551:

40

AAACATCGTT TATTCATCCA GCAGTGTGTC TCAGCTCCTA CCTCTGTGCC 50

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG 100

GGGAGGGGGT CATTGT 116

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT 50

CAGTATCGCT CCTCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG 100

20 TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT 150

(2) INFORMATION FOR SEQ ID :553:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50

GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTGCATGAC TCTACTATGG 100

GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150

40 NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT 189

288

(2) INFORMATION FOR SEQ ID :554:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50
15 GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100
GAATAAATTA CCTGTTTAAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC 198
20

(2) INFORMATION FOR SEQ ID :555:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAC TGAAGAACTT 50
35 GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG 97

(2) INFORMATION FOR SEQ ID :556:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

289

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAAACTTCA TCCTCTTGTT 50
GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA 100
10 GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCCTAGG 150
CTGTTCAGGT CTCCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT 200
15 CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT 250
CTTCAAGGGT GATCTTGTT 269

20 (2) INFORMATION FOR SEQ ID :557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :557:

ACTCCCTCAA GGTGCTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG 50
ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT 100
35 GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AGAAGAAAC 150
AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG 200
ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC 245

40 (2) INFORMATION FOR SEQ ID :558:

290

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10

GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC 50

ACAACCTTCG TTCCGCAGTT CATTAAATCCG ACTCTGATGC TAAGGTGACA 100

15 GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT 150

GGATTCTCT CTGTATCTTA AGAGTTATCA GAT 183

(2) INFORMATION FOR SEQ ID :559:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30

GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG 50

AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA 100

35 TGCTNAAGAA GCTGAC 116

(2) INFORMATION FOR SEQ ID :560:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

291

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC 50

TGGATACGGC GACGGTTTCT CATTTGCCTT TGTCAGCTCT CATTCGCTGA 100

10

GAGGCATAGA CCTTTTGGAT ATCATCAGGC TTTCCGTTTT TAGGAGCAAA 150

ACAGCTTCTT 160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC 50

AAATGCACCC CGTCCCCTG TGCGAGATCG TTTGAATNAG ACCAGAACT 100

30

G 101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTTCGAT 50
5 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100
TATGAGGAGT GGAATTTTAG ATGTCTATTA CATNGTCTT TTAAAAGAAA 150
AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183

10

(2) INFORMATION FOR SEQ ID :563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :563:

AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC 50
25 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTGCGTA 100
AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150
GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187

30

(2) INFORMATION FOR SEQ ID :564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :564:

293

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA 50
CACAGAAAAA TGGAAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT 100
5 GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC 150
AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC 200
AANGTGACTA TTC 213

10

(2) INFORMATION FOR SEQ ID :565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :565:

TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50
25 GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG 100
CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT 150
TTCTTTTTTT CCTTTAA 167

30

(2) INFORMATION FOR SEQ ID :566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :566:

294

GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT 50
GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT 100
5 TTGTCGATGA ATTGAGCAAC TGAGAACG 128

(2) INFORMATION FOR SEQ ID :567:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :567:

GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTGGGA 50
20 AAGTAGTCCT CAATCTTCGA TTTCCAGCA AGGACTTTCT CAGCNAGCGA 100
TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT 150
25 GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG 200
NG 202

(2) INFORMATION FOR SEQ ID :568:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :568:

ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA 50

295

AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA 100

CGGGTTACTT TCAAGGAAGA GTTGT TTTGT GACAAATTCT ACTCTTGATC 150

5 TA 152

(2) INFORMATION FOR SEQ ID :569:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :569:

20 CAGGTCCGCG TGCTCTCCGC ACCACCCAC TTCATTCCGG CCAAACCAAC 50

CGCACCCCTG AATTTCTCCG CAAATTCCT GCCGGCAAGG TCCCAGCATT 100

TGAGGGGATG ATGGATTCTG TGTGTTTGAG AGCAACGCCA TTGCCTATTA 150

25 CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T 181

(2) INFORMATION FOR SEQ ID :570:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :570:

40 ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT 50

AACTGGACTG GCCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCCTCNNT 100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA 150

ATGCTTT 157

5 (2) INFORMATION FOR SEQ ID :571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA 50

AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTTGACC 100

20 AGGGTATGAT CTTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC 150

ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC 193

25 (2) INFORMATION FOR SEQ ID :572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA 50

GAAGGATTTG AGGAGGTTGG TGGAATTTGT TGAAGGAGAG GGCGAGGAAG 100

40 AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG 150

297

CTTTCCTGTT TTAAACATGA AAGTGTGGC

179

(2) INFORMATION FOR SEQ ID :573:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15 AGGACCTCTA AGACATCCTT ATGACGACAG TTTGTCCAA GGGGATATCC 50
ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTTAAAAAGA 100
TTTTATTCT GATCTTTTGG CGATCTTCTT CTGCCCATG NNGCTGTTAC 150
20 TTNGCNCGGG NACCGGTAA TTCTANCCGC TAGGTGTGC 189

(2) INFORMATION FOR SEQ ID :574:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35 GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG 50
TAAAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CAAAGAATCG 100
TCCTTTTTTG AACTATAATN CCCNCGGTT ATTTTACCAT CACAGTTTAA 150
40 ATGTATATCT TTTACGTCTC TACTCAGACC ATATTNAAA GGGGCGCCTC 200

298

ATTATGGGGC ACAGAACCTT TTAATAAGTC TCATTAAGAT CTGAATTTTG 250

GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50

CCTGAC 56

20

(2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT 50

35 CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100

CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT 150

CGTATCTT 158

40

(2) INFORMATION FOR SEQ ID :577:

299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG 50
GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT 100
CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG 150
AGTCTTCCTC CTGGACTTCT GGTCTTGTA GGCTGTGCTT CATGCTCTCC 200
TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA 250
CTTTG 255

20

(2) INFORMATION FOR SEQ ID :578:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :578:

GAGGAGTCCA TGCCATCCTT GATGGAAAAG AACTGAAGA GAAAAGACAG 50
CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAGA GAAAATATGA 100
CATGATATCT TTGCTTTTGA GTTCCTCAGC CTCTCTGAAT TTATTAGTTG 150
GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC 200

40

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC 250

TCTTGAGATA GTTTTGT TTTT 270

5 (2) INFORMATION FOR SEQ ID :579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA 50

20 GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC 100

TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG 139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATC AGAGGTGAAA 50

TGTTCCGATCC AATTTATTTT TTGATAAGT TTTTCTTTCC TATNCCTNTN 100

40 GTTTTGATAA TATAATAAAG AAGATGAGGG GCCCA: A TATAGAGCTC 150

CTGAGNGAGT TTTNGGAG 168

301

(2) INFORMATION FOR SEQ ID :581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC TGT TTGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA	50
TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT	100
TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC	150
CATTCTCCCT GGCTGCCAGC CTTGAAGTC AGAACACCAT GGGAAAATTC	200
AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA	242

20

(2) INFORMATION FOR SEQ ID :582:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :582:

GCATTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG	37
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35

(2) INFORMATION FOR SEQ ID :583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGG 50

ACAAGAAACA CTTACCAACA AAAATATTTT AACCAACCCCA AAATAACTTA 100

10 CTCACAAATA TGCAAATTA TCTATGGCAT AGTATTTTCG ACTCGATGAC 150

ATTTAGAGAT AAAAAATCAA ATGGAGCTT 179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

AACTGCCATG AAGTAACCTG AAGGAGGCGC TGA CTGGAGG GATTGATTAC 50

AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA 100

30 GCGGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT 150

TTGCGACCAC AATNCACCCT TCATTTCGTA ACTGCT 186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

303

(xi) SEQUENCE DESCRIPTION: SEQ ID :585:

5	ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAATA AACTACAAAC	50
	GCACTCACAT CGCTATAATC CTTTAAAGGA CTTAAACTTT ACTCCATTAA	100
	GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCCCTATA	150
10	CCTCGGAGAA CTTTCGCGTA ATAACCACGT	180

(2) INFORMATION FOR SEQ ID :586:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 15 | (A) LENGTH: 183 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :586:

25	ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTG GCTAANNNNN	50
	NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC	100
	TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG	150
30	AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG	183

(2) INFORMATION FOR SEQ ID :587:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 35 | (A) LENGTH: 280 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN 50
ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA 100
5 GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT 150
GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG 200
NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT 250
10 GAGACTGATG TGACNTTCCT GGGACTGNCA 280

(2) INFORMATION FOR SEQ ID :588:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25 GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA 50
CCCCAAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC 100
TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAAGT GTTAAGCCAC 150
30 AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT 200
TNTTTTGTG CTTTTTGGG TATTTTCATT AGTATTTTCA CAAATCTCAT 250
35 GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG 300
ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT 350
GNGNNGCANG CTTANCTATG A 371
40

(2) INFORMATION FOR SEQ ID :589:

305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10

GAGAGAGAAC ACTCCCTCC ATCCAGCAC TATGCACAGT TCACGGCTCA 50
TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT 100
GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA 150
TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT 184

(2) INFORMATION FOR SEQ ID :590:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30

GGGGGCCCCG CGTNCACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCTC 50
NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTTCATG GATANGGTGN 100
GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCTTN 150
AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG 200
CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT 243

40

(2) INFORMATION FOR SEQ ID :591:

306

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10

ATTCGCCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTACTGAGAC 50
NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN 100
NAAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAAACTTT CAAATTCGGC 150
CCCTTTNGGC NANGCCCAAC CANNCCCCC CCCTTTTNC CGNCCCANNC 200
TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC 247

20

(2) INFORMATION FOR SEQ ID :592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :592:

GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAAATGC ATACTGTTTG 50
ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT 100
CCANGGATTA CGTTGCAATG TCTTCAAAAA TAGANAATTC ATTTTATATT 150
TCTNGATGAA ATATAATACT ANCTNNGCTA CTTTGGGAA TGTGACAAAA 200
TACTATGATG ATTACAACCTC ATTAAAGCAT AAATNTGCAT GATTTAACTN 250

40

307

CATGTTCCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA 300
TTTANGGCNT NNGTGCTTTG TAATGATTG NCNTTAGGTG AAGGGNTACT 350
5 TTTNTNNTNC TTCNTAGTAG ATTNNGNTTN NTCTTTTAA GAGGANTCNA 400
NTTTCATGNG TAANCATCAT CTTT 425

(2) INFORMATION FOR SEQ ID :593:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20

CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC 50
GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA 100
25 CGCGTGTGAA CACATGCGCG CNNGCGGCNC GCGATNCAA GCTGAAATGT 150
GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAAACAA CAATGAATGA 200
ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA 250
30 ANCAAAAG 258

(2) INFORMATION FOR SEQ ID :594:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

308

(xi) SEQUENCE DESCRIPTION: SEQ ID :594:

	GACCCTAACA ATATGTACAA AAATATAAAA TGTAATAAAA AAATACAAAC	50
5	AAATTCCTT TTTAAAGTAC TTTAAGAAA AAAAGCAGGG CCTTGAAGT	100
	TTTGGTTCTT TTTCTCTCCC CTGTTGCAAA TTCTCATGGT TTGGGTGGG	150
	TGGTGGAGAG CGCGTGTCT CATGCGGGTGC CTGCCCACGT GGGCGGGCGG	200
10	CTCTCTACTC GAAGG	215

(2) INFORMATION FOR SEQ ID :595:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 272 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :595:

25	GGGGCTGGTT TGGTCATCCG AGATCATTAA AAATGGCTGA CCCTAACAAT	50
	ATGTACAAAA ATATAAAATG TAAATAAAAA ATACAAACAA ATTCCTTTT	100
	TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTTT	150
30	TTCTCCCCT GTTGCAAATT CTCATGGTTT GGGTTGGGTG GTGGAGAGCG	200
	CGTGTCTACT GCGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT	250
35	CGAAGGTGAC CACGTTTAGA TT	272

(2) INFORMATION FOR SEQ ID :596:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

309

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

GACAAACTGT TGACACCCGG AGGCCTAAAC GAGGATTCA GCTTCCATTA 50

TGCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG 100

10 AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT 150

CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC 200

15 CTTCCTCAAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG 250

(2) INFORMATION FOR SEQ ID :597:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA 50

30 AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT 100

ATCAAGAAAC CAGACTGTGA TGA CTGGGAG AGCGGGCTGA ATGCAATGAG 150

35 TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGA ACTGCAC 200

AAACTGGCCA CTGACAAAAA TGACC 225

(2) INFORMATION FOR SEQ ID :598:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

310

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTATAGAT TTTCATTCAC	50
AAAAAAAGTC ATTCACATT TACTACTATAC ACGTTATGAT ATAATACAGG	100
AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA	150
CGTGTTGTTT TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA	200
CACCAGGGAC	210

20

(2) INFORMATION FOR SEQ ID :599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC	50
AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT	100
AGAAGTGAAA AAAAAA	116

40

(2) INFORMATION FOR SEQ ID :600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC 50
CCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA 100
TGGCCTC 107

(2) INFORMATION FOR SEQ ID :601:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

25 ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTTAGC CAATGTTACC 50
GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAAGCA CAGAGTGAGT 100
TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC 150
30 ATTTTCTTTC CTTAGTGTAC CAA 173

(2) INFORMATION FOR SEQ ID :602:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

312

(xi) SEQUENCE DESCRIPTION: SEQ ID :602:

5 GGAAGAGAAC ACATACACGA GGACCACTAC CTGATGAGGA CAAGAGAGAT 50
GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT 100
CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA 150
GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC 200
10 AAGTACCCAG TAGGAG 216

(2) INFORMATION FOR SEQ ID :603:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25 GAAAAAACAA TCATGACAGC AACTCTCCTA ACCACAAAAA TCACATATGT 50
TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA 100
TTTCTAGGGC CTTTCTGGG GAAAGGTCA TATAATTTAG CATACATACA 150
30 TATTCAGTGA ATGCATTCAT ATATTACTAT ATAAACACTC TCAGCTACAA 200
TGGTAATATA ATG 213

35 (2) INFORMATION FOR SEQ ID :604:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

313

(xi) SEQUENCE DESCRIPTION: SEQ ID :604:

5 GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTTTC 50
TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGA CTGGACC TCTGGTCTCA 100
ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150
10 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200
CTTCAAGAAG AAGAGCTGC 219

(2) INFORMATION FOR SEQ ID :605:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25

AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50
CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100
30 NNGA 104

(2) INFORMATION FOR SEQ ID :606:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTACCAC 50
ANNTACAGAA TCTCCACCAT AGCATCAAAA CCAACTCTGA GGAAGTTCGC 100
5 ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA 150
TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA 189

(2) INFORMATION FOR SEQ ID :607:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20

GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA 50
GAGCTCGTAT TTATCCTTTG CTTTATNTG AGACCAAGCT AGCCCTGAGT 100
25 AATTTTANNT GGTTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT 150
GCCTTACGCA CATTCTTTN T 171

(2) INFORMATION FOR SEQ ID :608:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40

GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA 50

315

TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAACTGTG 100

ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA 150

5 TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA 184

(2) INFORMATION FOR SEQ ID :609:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :609:

GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGA CTTTG TATTCTCTGC 50

20

CTGTGATTTT CNNTTCTAAA TGAACTCCA TGTNNNAACC AGGACGAAGN 100

TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC 150

25

TCTGTTACAC TAGGTGTAGA GTTCCAGAAT GTTCTTTTGT T 191

(2) INFORMATION FOR SEQ ID :610:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :610:

GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT 50

40

GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT 100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGACT 150

AGGTATGATT TTATAGGNAT AA 172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT 50

T 51

20

(2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTTTC AAAAAATAAA ACAGTATCTC 50

35 TTAATCACTG 60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT 50

CCTGGGCGCA CAGCGAGACT GTCTC 75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA 25

25 (2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

30 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTA CT ATGTTCCGAT CTGTGAATAG CCACTGCACT CTAGCCTGGA 50

TAATATAGTG AGAACCCATC TC 72

40

(2) INFORMATION FOR SEQ ID :616:

318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10

TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG 50

GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA 100

15

CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG 137

(2) INFORMATION FOR SEQ ID :617:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :617:

GCAGGGCAGT CTTGGTGTGC AGCCCCTCTC CTCTCTGTCC CCTGACACTC 50

30

CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT 100

CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTAC 139

35

(2) INFORMATION FOR SEQ ID :618:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

319

(xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5 TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG 50
TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG 100
CCTNCNCTGA GGNCNGCCAG GCCATTGTTG ACACCNNCAC CTCTCNNCTG 150
10 ANNNNCCCAA CCAGCCCCAT TNCCAACA 178

(2) INFORMATION FOR SEQ ID :619:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :619:

25 ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50
TTCTGCGGCC GCCACCGCGT GGA 73

(2) INFORMATION FOR SEQ ID :620:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40 TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA 50
AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT 100

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

(2) INFORMATION FOR SEQ ID :621:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15 TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCCT 50

GGAAATGAGC TAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNNCC 100

CACTTCCTCC CATGCCCTCC AAA 123

20

(2) INFORMATION FOR SEQ ID :622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :622:

CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA 50

35 AAAACATTTC NNGAGGAATT TTCAATTTCC AGCTTAAAGA ACNNNCCCAC 100

CAACATAACC AATTTATGAA ANNNAATTCA TAAAAGGTA TAGAACCTCT 150

TGTNNNCATG ATGGCAAGGG ACA 173

40

(2) INFORMATION FOR SEQ ID :623:

321

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10

TTTATTGTAT CATGAGGCAT TGAACATCT GAATAATCA ATGTCTGGGC 50

GGTGAAGGCA GCTGCTTCT CCTTCACTTC TTTGGGTAC TAGAGCAACT 100

15

TGTCAGTAGA TT 112

(2) INFORMATION FOR SEQ ID :624:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :624:

ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGGC 50

30

GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100

AGGTCTGCAT CCCCTCCCC 119

35

(2) INFORMATION FOR SEQ ID :625:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

322

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

10 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20 ATAAAAATCT GAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG

50

35

AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGGCGA GTGCGGCCTC TAGACAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :628:

AAAAGAAGTA GGTCTGTCTG TTCTGGTTGC CCTAAGAGAA GAAGANNNGC 50
GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA 100
CCGGCAGC 108

(2) INFORMATION FOR SEQ ID :629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :629:

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA 50
CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA 95

(2) INFORMATION FOR SEQ ID :630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

CCAGCNCCGA AAAGCCAAGA CTTTCATCAAC TACATAGGTC TTACCATTGA 50
5 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100
AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTG 139

(2) INFORMATION FOR SEQ ID :631:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20

CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC 50
TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA 100
25 GCTGAAGTGG TGTGCTT 117

(2) INFORMATION FOR SEQ ID :632:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :632:

CCAGCNCCGA AAAGCCAAGA CTTTCATGAAC TACATAGGTC TTACCATTGA 50
40 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100

325

AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTGA GGCCGCCATT 150

GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA 50

ACAACCTAGA TGTGAAAACA GAATAAATT CACCCAGAAA AACAAAC 97

20

(2) INFORMATION FOR SEQ ID :634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTGCACC 50

35 TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100

TTCTTCCTCA GGAATAGACT CAAGTATGCC TTGACTGGAG ATGAGGTAAA 150

GAAGATATGT ATGCAACGTT CATTCAAA 178

40

(2) INFORMATION FOR SEQ ID :635:

326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10

CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC 50

CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA 90

15

(2) INFORMATION FOR SEQ ID :636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :636:

CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG 50

GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC 100

30

T 101

(2) INFORMATION FOR SEQ ID :637:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

327

(xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT 50

5 TTTAATAAAG CACAGCACAA 70

(2) INFORMATION FOR SEQ ID :638:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :638:

CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA 50

20 ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG 100

TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC 150

25 TCGGAGCTCG 160

(2) INFORMATION FOR SEQ ID :639:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :639:

CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC 50

40 CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC 100

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

(2) INFORMATION FOR SEQ ID :640:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15 CCGACCACCC CTCCTTTTC TTCGTCCATC CAGCACAGCA AGACCAACGG 50

GATTCTCTTC TGCGGCCGCC ACCGCGTGGA 80

(2) INFORMATION FOR SEQ ID :641:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30

AACTAAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA 50

GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA 100

35

(2) INFORMATION FOR SEQ ID :642:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

329

(xi) SEQUENCE DESCRIPTION: SEQ ID :642:

AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA 50
5 GTTAATGTTC CATCCATGCT GCTTAAA 77

(2) INFORMATION FOR SEQ ID :643:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT 50
ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG 100
GGCTACAAGG ACTCGCCCTC CGTCTGG 127
25

(2) INFORMATION FOR SEQ ID :644:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :644:

GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT 50
40 GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA 100
AAGTTTATTT TAGACC 116

330

(2) INFORMATION FOR SEQ ID :645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTCG GGTTTTCCAG 50
GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC 100
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATACAAG 150
ACACTCAAGA CAGCAATTAA TCTGTCATCA TT 182

20

(2) INFORMATION FOR SEQ ID :646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA 50
ATAAAAATCT GAAAAC 66

35

(2) INFORMATION FOR SEQ ID :647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

331

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT 50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT 93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTGT TCCCCACTGA GATGTATGAA GGTTTGGTC TCCCTGGGAG 50

25 TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA 100

AAAGTGCACA CCTT 114

(2) INFORMATION FOR SEQ ID :649:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

40

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG 50

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50
AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100
GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATTT 150
20 AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs

333

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :652:

CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTTTA	50
AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT	100
CTCGAGGACC TGGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA	150
TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG	198

(2) INFORMATION FOR SEQ ID :653:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :653:

CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG	50
ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG	100
GCATCTTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA	150
TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTG	200
TTGCTATAAT AACACTTTTC TTTT	224

(2) INFORMATION FOR SEQ ID :654:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs

334

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :654:

CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT	50
GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC	100
CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA	150
AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTGGGTTT	200
CTGAGCGCAT AAAGCTAAGG AGGGGT	226

(2) INFORMATION FOR SEQ ID :655:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :655:

30

TTAAAAAAT TCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTCA	50
TTTGGTAACC TGTTTAGAAT TATAAAATC ATTTCATTTG GCCCAGCCCA	100
TACGCCCAAG AGAAACTTC CAGACTTTTC TGATGCCATC CAGTTTTGTT	150
CTTACAAAAT GCATATT	167

(2) INFORMATION FOR SEQ ID :656:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

335

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT 50
10 TCTGCGGCCG CCACCGCGTG GA 72

(2) INFORMATION FOR SEQ ID :657:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

25 AGAGGGTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA 50
TACAGAACAA AAAAAGTTTC CCTTTTAACT ACTAATGTTA CAAATCTGTA 100
TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAAT AAGGTGTATA 150
30 GTACAATGTA TTCTAAAGT GTTCCGCC 178

(2) INFORMATION FOR SEQ ID :658:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50
20 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAACTTC TTTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50
TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT 100
AAACACTGAT CAACTCAGT TGTCTTACG TTAGCATTAC TCTGTCATAG 150
40 C 151

337

(2) INFORMATION FOR SEQ ID :661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :661:

AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAACCTCAG CCACGTCTCC 50

15 TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT 100

CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG 150

TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC 200

20 TTCACTGTGC CTGCTGAGTC AGCTTGCATC TCGGCCTTCG GTGCG 245

(2) INFORMATION FOR SEQ ID :662:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :662:

35 GCCAGCGCCG AGGTGCGATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50

AATAAAAACM TGA AACACC CC 72

(2) INFORMATION FOR SEQ ID :663:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

338

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTGCTTAT CACTCTCCCC 50
AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :664:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCG 50
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150
CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200
CGGATAGTCA CACTCCCTGC CGA 223

35

(2) INFORMATION FOR SEQ ID :665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

339

(xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
AATAAAAATC TGA AACACC 70

(2) INFORMATION FOR SEQ ID :666:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC 100
TTTCTACGTA CCGTATAG 118

25

(2) INFORMATION FOR SEQ ID :667:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :667:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC 50
40 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :668:

340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTGATCTTC AACTCTGCAT 50
ACAAGCAGA 59

15

(2) INFORMATION FOR SEQ ID :669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :669:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50
CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200
CTGCTCCCAG AGCCCACTTT TTT 223

35

(2) INFORMATION FOR SEQ ID :670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

341

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

10 (2) INFORMATION FOR SEQ ID :671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:

20

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :672:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35 GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

(2) INFORMATION FOR SEQ ID :673:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

342

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :673:

GCCTGCGCCG ANGCAATCCC TTGACCTGA GTCTGCAGCA GGTCCCTTTT 50
10 GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100
GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC 150
15 CAAAGTATTA AAAGCAACTT TGCAATT 177

(2) INFORMATION FOR SEQ ID :674:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
25

(xi) SEQUENCE DESCRIPTION: SEQ ID :674:

30 GCCTGCGCCG AGCACAAGAC AATGACGAAC ATTTTAAAAA AAAAGAATGA 50
CGCACATTTT AATAAAGCAC AGCACAA 77

(2) INFORMATION FOR SEQ ID :675:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

343

(xi) SEQUENCE DESCRIPTION: SEQ ID :675:

GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG 50
5 CCGTAACTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC 100
ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACACA CCGATTGCAT 150
AAAATCTTTT TTTAGGAAAA AAACAC 176

10

(2) INFORMATION FOR SEQ ID :676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :676:

GCCAGCGCCG ACGCCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG 50
25 CCGTAACTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT 100
ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C 141

30

(2) INFORMATION FOR SEQ ID :677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :677:

CTCTGAACAG ACACGAAGCT GCCCCTCGTA CAGCCACTCG GCGGCTGACC 50

344

ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG AACTGTCACG 100
CTGACAAGCG CCTCCGCGGC GGCTCGGAGC CGGACTCAGG CGGATCTTGA 150
5 CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCGC GTGGACCTAG 200
GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCCCTGGAC 250
CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT 300
10 CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA 350
TCCAGGTGCT GTAGA 365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50
CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC 100
30 GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAGGCA GATCTTGACA 150
GCCTTGCCCCG CGAGTGCCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG 200
TGACTGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCC GCGGAC 250
35 CTGCCGGAGA ACAATACCAC CGCCGCTNT GCCGCAGTCT TTCCCGGAGG 300
TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TGCGTGCGGT 350
40 CATCTAGGTG CTGTAG 366

345

(2) INFORMATION FOR SEQ ID :679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :679:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50
CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA 100
GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC 150
CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT 200
TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC 250
TTG 253

25 (2) INFORMATION FOR SEQ ID :680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :680:

GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG 50
GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC 100
CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT 150

40

346

CAGCCTGGGA TCCGGTGACG GCCTAGGCG AGGCTGGGCC AGGAGTCCCA 200
AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA 250
5 GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCTACGG GCTC 294

(2) INFORMATION FOR SEQ ID :681:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :681:

CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGCGC 50
20 GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG 100
CTTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC 150
25 TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC 200
TGCCAACCAG AACTGACACG CGACCTCCTG GGCCTGACG CCATTAAAC 250
CAACGTTGGC GCGCGGCG 268
30

(2) INFORMATION FOR SEQ ID :682:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 40

(xi) SEQUENCE DESCRIPTION: SEQ ID :682:

347

GCCACCGCCG AGGAAAACCG TGCCTGTGA GCCATGATCA ACCCCACCGT 50
GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG 100
5 AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA 150
AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTTCCTGCT TTCACAGAAT 200
TATTCCAGGG TTTATGCGCC AGGCTGGTGA CTTACACAGC CATAATGGCA 250
10 CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC 300
CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA 350
15 TACA 354

(2) INFORMATION FOR SEQ ID :683:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :683:

CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCT CTCCTCTCTG 50
30 TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC 100
AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT 148

35

(2) INFORMATION FOR SEQ ID :684:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

348

(xi) SEQUENCE DESCRIPTION: SEQ ID :684:

5 AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA 50
CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG 100
CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG 150
10 GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA 200
TGCTCTTGCC AACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC 250
TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT 300
15 GTGAGGC 307

(2) INFORMATION FOR SEQ ID :685:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
25

(xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30 CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG 50
AGCTTCTCCC CGTGAATCAC ATGCCGAGAG TCCCACTCTT AGCTGGCAAA 100
TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA 150
35 GGAGCCATCT CTAGCGGGCC CTTC 174

(2) INFORMATION FOR SEQ ID :686:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid

349

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA 50
CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTTACT 100
TATAAA 106

15

(2) INFORMATION FOR SEQ ID :687:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTCCCCCA 50
GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA 97

30

(2) INFORMATION FOR SEQ ID :688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50
CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA 100
5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150
GAATAGAGTC TAAGCGAACG AC 172

(2) INFORMATION FOR SEQ ID :689:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20

GCCACCGCCG AGCTCACCCC TGCGGTGCAC GCCTTCCTTG GACAAGTTT 50
TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100
25 TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC 150
CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTA AGCGAGTAGC 200

(2) INFORMATION FOR SEQ ID :690:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA 50

351

ACACAAATTC ACAAGTGNTC TCAAAAAACT C

81

(2) INFORMATION FOR SEQ ID :691:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15 TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA 50
TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG 100
TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCTTCT 150
20 GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TTCGACTTCA CTCCATAAAC 200
AGCTGACGCT CAAAAAG 217

25 (2) INFORMATION FOR SEQ ID :692:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTTCCGCACC TCCAAGGGGA 50
GAAGAGTAAG AGACAGCTTT CA 72

40

(2) INFORMATION FOR SEQ ID :693:

352

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC AGGGGAAGCA 50

GAAAAAGGCA AACAAGAAGA AGGAGGAACC CAAGCAGCTT TCGGGCTTCG 100

15

CGTCCAACCC TCTTGCCCTT CACCTACGCG CCTAGAGCCA GTCCCACCAC 150

GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTC 200

CCTTTGACCT AAGCCTACAG CAGGCCCCCTT TTGTGCTTCC TTCCCCTCAG 250

20

GCAGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTTGTCTTC 300

CCGATGCTTT TTGTTACCGT GGGGTTTGC 329

25

(2) INFORMATION FOR SEQ ID :694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :694:

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGG CCTGCGCCGA 50

ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGCC CACGGATCCG 100

40

GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG CTGCGGACCA 150

353

GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA 200
AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG 250
5 AGCCCACTTT TTTTTTTTTT TTGGAATAA AATAGCCTAT CTTTCG 296

(2) INFORMATION FOR SEQ ID :695:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :695:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG 50
20 AACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGC GCAGAGG 100
CGTGTCTTAG CACTAACCTC CTCCCTAGCC CTTATTTGG TGGCAGAAGT 150
25 GGCCTCCACC CCTTCACCGT TAAAAATAC TCCGTGGAGA AAAGAAAGCT 200
TNAAGGAGTA G 211

(2) INFORMATION FOR SEQ ID :696:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :696:

40

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC 50

354

CCAACAACAC AGACGGCGAA AACAAACAA ACTTAAACCT AG

92

(2) INFORMATION FOR SEQ ID :697:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15 GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC 50
CTACCAGCAA GGGGTCCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG 100
GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC 150
20 ATAGTCAAGA GAAAGGATT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA 200
GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT 250
25 CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC 300
GCATGCGTAC CTGT 314

(2) INFORMATION FOR SEQ ID :698:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40

GCCACCGCCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT 50

355

GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT 100
CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCT 150
5 CCTTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC 198

(2) INFORMATION FOR SEQ ID :699:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :699:

20 GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG 50
CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAGTGA ACAGAATGAC 100
CTTCCTACGC ACAACACAAA CACCAGTTAA TGCTCCATCC ACGCTGCTTA 150
25 AAGAGCATTG CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCACCC 200
TTAGCCGGCA TGCTTACATT AATAGCTAGA 230

(2) INFORMATION FOR SEQ ID :700:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :700:

AGCAACAAAA ATGTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT 50

356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC 100
AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAA GAGCATTCCT 150
5 GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCCACCCTC ACTTGGCATG 200
CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA 250
GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC 282

10

(2) INFORMATION FOR SEQ ID :701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCAA 50
25 CATGGATCCG AATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC 200
30 CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAAATAAA ATAGCCTGTC 250
TTTCG 255

35

(2) INFORMATION FOR SEQ ID :702:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA 50
CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC 89

(2) INFORMATION FOR SEQ ID :703:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCCTA 50
GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

(2) INFORMATION FOR SEQ ID :704:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35 GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA 50
ACACGGATCC GAATCACCTG GCCCGAAACC ACCTACCTAG CCATGATGAA 100
40 TGCTGAGGAC CCAGATGCAG TAC 123

(2) INFORMATION FOR SEQ ID :705:

358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10

GCTTGATGCC TGCGCCGAAC AACATACAG AATGCGGCGA GTCCCTCTGG 50

ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT 100

15

GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCCC 150

ACATCACC GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG 200

GACTAACCCT GTTCCCAGAG CCCACTTTTT TTCTTTTTC GAAATAAAAC 250

20

AGCCTGTCTT TC 262

(2) INFORMATION FOR SEQ ID :706:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35

GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG 50

AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG 100

CGTGTCTTAG CACTGCCCCC CTCCCTAGCC CTTATTTGG CGGCGGAAGC 150

40

GGCCTCCACC CTTCCCTGT TTGCAACAC TCTGCGGAGA AAAGAGGACT 200

359

TCAGGGAGT

209

(2) INFORMATION FOR SEQ ID :707:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15 GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC 50
TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAGA AGAAGGAGGA 100
ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTTACCTGT 150
20 GAGCCTGGAG CCAGTCCCAC 170

(2) INFORMATION FOR SEQ ID :708:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35 GCCACCGTCG AGGATTCAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCCG 50
ACGTTCCGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT 100
TCTGCAGGCC GTTTCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA 150
40 CCCAGAACCT 160

360

(2) INFORMATION FOR SEQ ID :709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AACTAACT GCAAACCTCT 50

15

G 51

(2) INFORMATION FOR SEQ ID :710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

30

CAGGATTCTC TTCT 64

(2) INFORMATION FOR SEQ ID :711:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT 50
5 CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC 100
TGGG 104

(2) INFORMATION FOR SEQ ID :712:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20

CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT 50
TTGTTTTTAG TTGAAGGC 68

25

(2) INFORMATION FOR SEQ ID :713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :713:

AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100
40 GTGCTTGGGT CGCTGTCTAC TGCTCCT 127

362

(2) INFORMATION FOR SEQ ID :714:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC 50

15 CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT 90

(2) INFORMATION FOR SEQ ID :715:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA 50

30 ACAAAAATCT GAAACATC 69

(2) INFORMATION FOR SEQ ID :716:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA 50
5 CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT 100
AA 102

(2) INFORMATION FOR SEQ ID :717:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20

AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100
25 GTGCTTGGGA TACGCTGTCT ACAG 124

(2) INFORMATION FOR SEQ ID :718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA 50
40 TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGCAG 100

364

ACAAGGTCCC AAAGACAGCA GAA

123

(2) INFORMATION FOR SEQ ID :719:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15 ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50

TTCT 54

(2) INFORMATION FOR SEQ ID :720:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30

GACCACAGGG CCTTCAATCC TTTTGTGTTT TCAACAGTCT TGCTGAATTA 50

AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT 100

35 AATAAACTG TGCACTC 117

(2) INFORMATION FOR SEQ ID :721:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25 ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA 50

40

TCCCC 55

366

(2) INFORMATION FOR SEQ ID :724:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :724:

GTGTACTATT AGCCATGGTC AACCCCACCG TGTTCTTCGA CATTGCCGTC 50
15 GACGGGCGAG CCCTTGGCGC GCGTCCTTTG AGCTGTTTGC AGACAAGGTC 100
CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA 150
TTTGTTATA AGGG 164

20

(2) INFORMATION FOR SEQ ID :725:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :725:

GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC 50
35 ACACCCTCAA CCGTTGCTCC TGTA GCTTCC GAGTCCTGGT GGTGTCGGCC 100
AAGTTCAGTA 110

40

(2) INFORMATION FOR SEQ ID :726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs

367

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :726:

CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTCTTC GACATTGCCG	50
TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG	100
TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
TTTGATTATA AGG	163

(2) INFORMATION FOR SEQ ID :727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :727:

GAGGGCGACT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA	50
GTCAGTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC	100
CTGTT	105

(2) INFORMATION FOR SEQ ID :728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

368

(xi) SEQUENCE DESCRIPTION: SEQ ID :728:

5 GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50
ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100
AGGAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTCGA GGCCGCCACT 150
10 GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA 186

(2) INFORMATION FOR SEQ ID :729:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :729:

25 GCCAGCGCCG AGGTTGCATA TTCTAGGCGC AGGTATATGA TTGCCATATA 50
ATAAAACCT GAAACATCC CACCCGGGAA AAAAAAAAAA AAAAAAAAAA 100
AAAAACACCC CCCCCCACA AAAA ACTCAA ATTCCCCTCC CAAAAACCC 150
30 CCTCAAAATC AAAAAC 167

(2) INFORMATION FOR SEQ ID :730:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :730:

369

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCT 64

5 (2) INFORMATION FOR SEQ ID :731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- 10 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCCGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96
20

(2) INFORMATION FOR SEQ ID :732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- 25 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

35 CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA 84

(2) INFORMATION FOR SEQ ID :733:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA 50

25 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCCACT 50

40

AGCACCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTT TGCCGGG 97

371

(2) INFORMATION FOR SEQ ID :736:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT 50
15 GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA 100
TACAGCATT ACAAACCGC GCATCTC 127

(2) INFORMATION FOR SEQ ID :737:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :737:

30

GCCTGCGCCG ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA 50
CAGGATTCTC TTCT 64

35

(2) INFORMATION FOR SEQ ID :738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

372

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

5 GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :739:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG 50
CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG 95

(2) INFORMATION FOR SEQ ID :740:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35 GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA 50
GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA 100
40 CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCGAAGGA 150
CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT 200

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA 245

(2) INFORMATION FOR SEQ ID :741:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15 GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTCGTCTAT CACTCTCCCC 50
AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :742:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 242 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30 GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC 50
GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA 100
35 CTCTGATAGT CTTCATTCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG 150
AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT 200
CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA 242

40

(2) INFORMATION FOR SEQ ID :743:

374

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

(2) INFORMATION FOR SEQ ID :744:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :744:

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAAACAT

69

30

(2) INFORMATION FOR SEQ ID :745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :745:

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT 50

AATAAAAATC TGAAAACATC CCAC 74

5 (2) INFORMATION FOR SEQ ID :746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50

AACAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG 88

20

(2) INFORMATION FOR SEQ ID :747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50

35 AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :748:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT 50
GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG 100
10 GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATCCCGTG GGGCTCACCC 150
CAAAGCATTAA AAAGCAGCTT TGCAATTC 178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50
ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100
30 AGAAAGGCAT CTTTCGCCAG TGGATTCGCC CCAAGGTGA GGCCGCCATT 150
GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT 200
35 TGGCGCTGCT GCCTATAACA AACACTTTTT TTTT 235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTTC ATCCAGAAAA GCAAGAGAAA 50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT 87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG 50

25 GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC 100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC 150

ATGCCAAAGA CACTCAAAGA 170

30

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50

AATAAAAAAA TGAAAACACC CC 72

5 (2) INFORMATION FOR SEQ ID :753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGCGCCG AGGACACCAA GAAGGTTTTG GACAGCGTGG GCATCGAGGC 50

GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAACA 100

20 TTGAAGACGT TATTGNCCAG GA 122

(2) INFORMATION FOR SEQ ID :754:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACGCGCG ACTGAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA 50

GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC 100

AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG 150

40 GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG 200

379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

(2) INFORMATION FOR SEQ ID :755:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15

GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT

50

AACAAAAACC TGAAAGCATC A

71

(2) INFORMATION FOR SEQ ID :756:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30

GCCACGCGCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

35

TAGTGCTTTT TCAGTGGGGC GGGGCGGGAA GCAGGCGGGA CCAGGCAGCC

150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA

243

40

(2) INFORMATION FOR SEQ ID :757:

380

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCC 64

15

(2) INFORMATION FOR SEQ ID :758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG 50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT 100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC 150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA 200

35

GACGTCGACA ACCAGAACTG ACGTGCACC TCCCGGGCGC CGA 243

(2) INFORMATION FOR SEQ ID :759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG 50

AAGATCACGC TCCCCGCCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT 100

10

CTTCGCTCTC AGCTCCCCCT GTCCCTCAG CTCCAGACGT AGGGGAGGGG 150

TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA 200

15

TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTC GGCCA 245

(2) INFORMATION FOR SEQ ID :760:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50

30

AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :761:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

382

(xi) SEQUENCE DESCRIPTION: SEQ ID :761:

GCCAGCGCCG AGGTGCGATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50
5 AATAAAAACT GAAAACACCC C 71

(2) INFORMATION FOR SEQ ID :762:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :762:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50
20 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :763:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35 GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCGA 50
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150
40 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200

383

CGGATAGTCA CACTCCCTGC CGA

223

(2) INFORMATION FOR SEQ ID :764:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50

AATAAAAATC TGA AACACC 70

(2) INFORMATION FOR SEQ ID :765:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30

GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50

TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC 100

35 TTTCTACGTA CCGTATAG 118

(2) INFORMATION FOR SEQ ID :766:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50

AACCAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50

25

ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

40

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG 100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

5 CTGCTCCCAG AGCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37

20

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35

(2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

386

(xi) SEQUENCE DESCRIPTION: SEQ ID :771:

5 GCCACCGCCG ACTCCAGGCA CTCACTCAA CTGATCTTC AACTCTGCAT 50
ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :772:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :772:

20 GCCTGCGCCG ANGCATTCCC TTGACCTGA GTCTGCAGCA GGTCCCTTTT 50
GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100
GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC 150
25 CAAAGTATTA AAAGCAACTT TGCAATT 177

(2) INFORMATION FOR SEQ ID :773:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :773:

40

AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA 50

387

GAATTAGAGG TAAAGGAATC CTAAATATAA GAGCACAGCA GCAATCACAC 100

TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG 150

5 T 151

(2) INFORMATION FOR SEQ ID :774:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :774:

ATCTTAATGA ACATGGCATT TAAATCCTG TAATTCAAA CAGTGAACCA 50

20

CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA 100

CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCGAGTCT AAAGCTACAC 150

25

ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG 200

GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG 250

AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA 299

30

(2) INFORMATION FOR SEQ ID :775:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG 50
TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA 100
5 AACCGTATAT TTAATGAA TTACTAGACA GGAATGTAA TCATGGCAA 150
AGAAATTAAG TTTAAGAAG ATGCTAGTGC TAAGC 185

(2) INFORMATION FOR SEQ ID :776:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :776:

20

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA 50
TTTCACCACA CATGGCAACA AACTTACCTT CTTAAGAGC GGCAGTAATC 100
25 ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA 150
AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT 200
CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC 250
30 AACAT 255

(2) INFORMATION FOR SEQ ID :777:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

389

(xi) SEQUENCE DESCRIPTION: SEQ ID :777:

	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTCAT AAAGTAAGTT GAAAATTTCTG TTCTTGGCTG AATCGTGTTA	100
	AACCGTTGTA CACAACGTAG TAAAATTCAT AACCCATCTG CATACCAATC	150
	GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239

(2) INFORMATION FOR SEQ ID :778:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 252 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25	ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTCGA ACATGCTACA	100
	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG	150
30	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTAAAGG ATGACTCAAC TTCGCCAACT CGGTTCTCTCA TTAGGACAAC	250
35	TA	252

(2) INFORMATION FOR SEQ ID :779:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 265 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

390

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

TCGGATTTAT	ACGGCTGTTA	GTGCTATCGG	CGTCTGGTAT	GTGTTATATA	50
TCGCCTATCG	TTTTTTGGCC	AATGGGCGTT	GGCTACGCGG	GGCAATGATT	100
10	GCCATCGTTT	TTGTTATCTT	GACTTATTTT	GTCATTTTAA	150
	ATATTATTTA				
	ACTATTTTAC	AAATAAAGTG	GTCAAATGGG	ATATTTTGCC	200
	AAAAATAGAG				
15	AAAGTGTTAG	GCGGCCACACA	GCTGGAGGAA	GAGAAAGCGG	250
	CTGTGCATGA				
	AGTTATTGCA	CCCGC			265

(2) INFORMATION FOR SEQ ID :780:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :780:

30

CTCAGCTGGA	CCAAATTAGT	TGAATTACTC	ACCATCAATA	AACTATAAAT	50
GGCGCCAATG	ACCAACCCGC	CAACGATTCC	CGTTGTCAAA	GAACCTAATA	100
35	ACAAGTAACC	AACCGCAGCC	CCAACAAGCC	CAACTAGGTT	150
	TAAAAAAACC				
	AAGCAAAAGG	CCAACTGTCC	GTCGTTTATT	GGATTGTATC	200
	TGCTCATATA				
	ACATTAAAC	TTAACCGTTG	GCACTTCTTT	CTCAGACCCG	249
	CCGATACTG				

40

(2) INFORMATION FOR SEQ ID :781:

391

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :781:

10

GAGAGAACCC ACCATAGTAC TGTCTCTGC AGACAAGACC AACGGCAAGG 50
CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC 100
TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC 150
TTCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA 188

(2) INFORMATION FOR SEQ ID :782:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :782:

30

AATATTTATT TCATTTGTTT ACTACCACTT CATTTTATTT GTTTGCTGCT 50
GCCGTTTTAT TTATTTTAC TGAAAGTGAG AGGGAACTTT TGTGGCCTCC 100
AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTGG AACATCTAAC 150
AAGCTGAAGN GGAAAAGGGG GTTTCGCAA AT 182

(2) INFORMATION FOR SEQ ID :783:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

392

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :783:

20 CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC 50
10 CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT 100
CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT 150
15 TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA 200
CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG 250
AGAGAATTCA AATGCGTGTT GGTGTTCCCTG TTAGTACAAG CAGCA 295
20

(2) INFORMATION FOR SEQ ID :784:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :784:

CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC 50
35 GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCAC TCAAGACCAG 100
TACCTGATGT TGTGGAATG GCAACCATT GTGTCAAACG CACTGGTAGA 150
ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTTGTT TATTTCCATG 200
40 AACAAATCCT TGATACCTC TTCGTCTGAC AAAATACCTT CGTGACGTGT 250

393

TGAGTATTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

(2) INFORMATION FOR SEQ ID :785:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :785:

15 GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA 50

CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTTC 100

ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC 150

20

CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA 200

GCGCTTTGAA TACTGTTCTG GGTTCACGGT GGAGATCTCC GCGCAGCCAT 250

25 GTTTAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA 300

GTA 303

(2) INFORMATION FOR SEQ ID :786:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :786:

40

TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT 50

394

CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT 100
ACATGAAGAA TGATGGTGTT CGTGGGGCCA TTAAGTACTA AGCCAAGAAG 150
5 TTATCACGAC AACCTATAAC TTGGGCCGAA TTAAGTTGAT GATGCACGGG 200
GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA 250
CTGGC 255

10

(2) INFORMATION FOR SEQ ID :787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :787:

CATTGAAAAG TGCCTGAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG 50
25 TCAGAATCAA CAAACTAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG 100
GGCATGATAC AAACCACTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG 150
ACTTATTTTT ATTTTTTTTT TTTTGGACAG ACTCCCTTTG TCCCCAGGCC 200
30 GGAGTG 206

(2) INFORMATION FOR SEQ ID :788:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

395

(xi) SEQUENCE DESCRIPTION: SEQ ID :788:

ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT 50
5 CACGTGGTTC ACCTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG 100
TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTTCAAAC GAGGCGTGGA 150
AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG 200
10 GAACAATTCC GCGACACCCT TCGTCTGACA AAAAACCTTC GTGACGCGTC 250
GAGTATCCGC 260

15 (2) INFORMATION FOR SEQ ID :789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC 50
TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT 100
30 GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCCGCACT 150
TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG 200
35 ATCGACGC 208

(2) INFORMATION FOR SEQ ID :790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double

396

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

AAAAGAAGTA	CGGTAAGGCA	AATCCTGAAA	TTAAGAGTTA	CTATGTGCCT	50
GAAAATACAT	TGTTCTACTC	ATTTAGTGTG	ATGGCAATGG	GCGCCGGCGC	100
10 ACTCTTGCTA	TCGACCATCG	TCGCGCTTTG	GATGAACCGT	CGTAAGTCAC	150
AATTAATGTA	GACACAACGT	CGATTCTCGT	GACTTATGGG	GATCGCAACT	200
15 TTCGCGCCAT	TCTCGATCAA	CACAGCCGGT	TGGTCAGTGA	CTGAATTAGG	250
TCGTTATCCA	TGGGTGTTT	ATGGCTTGAT	GCTAATAGC		289

(2) INFORMATION FOR SEQ ID :791:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	232 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
25 (D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :791:

30

TTTCCTGTGG	AAGTAGTTAA	ATTGATAAAT	TCCAAAAATT	TGGCAATTAA	50
TTGCTCATT	TTAATGGTAG	AGTTTCCATT	AATGAAGTTG	GAAAATACGG	100
35 TGAATCTTTC	AATGAACTCA	GTTAGACATT	CGGAATGAGC	TTCATACATT	150
GTCTTATTAT	CTTTCTTCAA	TTTATCCTCC	AAATCTGGGA	ATTCTGATAA	200
CCAAATTGAA	GCACCTTATC	TATGATCCGG	GC		232

40

(2) INFORMATION FOR SEQ ID :792:

397

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :792:

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC 50
TGGTAATATC GAACAAACTA TTTTAAAGAA CTTGATTCTT GGCAACATTA 100
AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG 150
GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA 200
TGCCTATTTT GCGAAGTATG GATCTAAATA AC 232

(2) INFORMATION FOR SEQ ID :793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTACGGTA GTGANCCCAG TGACCAGATG TCTTATACAA 50
GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA 100
ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC 150
ATTTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA 200
ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTCACGTTT TTTAGCTTCT 250

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT

292

(2) INFORMATION FOR SEQ ID :794:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15 CAGCAGGCAC AACACCATCG GTTGTGCTG AAAGTATTTT TAAGTCTTTG 50
GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACCTATG CGGGTATGCA 100
TGATGTCATT CCTGCATCCG ATGATTTTTA ATTAATTACA ACAACTGATG 150
20 ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA 200
GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC 250
25 CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC 288

(2) INFORMATION FOR SEQ ID :795:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :795:

GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT 50
40 CGATAGACCC AAAAAGTGTT TTAAGTGGAA AACACCTTAT GAGGTTTATT 100

399

TTGATGAAGT GTTGCAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT 150
CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTC 200
5 GAGGTCAGTT ACGGCGTCCA GTCTTTGAGC AGATGATTG CCCCAGTGA 250
TCGTCGGC 258

(2) INFORMATION FOR SEQ ID :796:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :796:

20

TGCTTCAAAG CCTGGCTTAA CCCGCTGCC CACCAACTTC AATTATACCT 50
GCCCCTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC 100
25 CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACA TTTAACACAC 150
AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG 200
AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG 250
30 CTCATGTAAC GCGACAATAT 270

(2) INFORMATION FOR SEQ ID :797:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

400

(xi) SEQUENCE DESCRIPTION: SEQ ID :797:

5 AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC 50
 TTGTGTAGGT TGTCTGAAAC GGTGCGAGTC ACCGGTTAGC TTGATAAGTC 100
 AGGTTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC 150
 10 AATCGCACTT TACATCATTAG AGACCCTTAC TAGAAGTAAC TGGCCATCCT 200
 GCCACCGCTT 210

(2) INFORMATION FOR SEQ ID :798:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :798:

25 ATCATAAGCG CTGGAAGTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT 50
 GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA 100
 CCACGGTCCA AGGCAGAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA 150
 30 TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCCCAA TAACGAGACA 200
 AGTAGTTGAG CTAAATGC 218

(2) INFORMATION FOR SEQ ID :799:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

401

(xi) SEQUENCE DESCRIPTION: SEQ ID :799:

5	CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG	50
	AGAATAGCAT TACCAAATGG AACAACTGTC TACAGTCAGG ATTAAAAAGA	100
	ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG	150
10	AACAATACAA CACTGAATTA CTCGGC	176

(2) INFORMATION FOR SEQ ID :800:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :800:

25	GCAATTGCTT AATTGTCTCT TCCTTCTTAG CATTTTGCTG AGAAGCCAAA	50
	CGTTGCGCCA ATTCAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA	100
	TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT	150
30	TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA	200
	GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT	250
35	TCGA	254

(2) INFORMATION FOR SEQ ID :801:

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 203 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

402

(xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5 ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA 50
TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT 100
AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT 150
10 AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA 200
ATG 203

15 (2) INFORMATION FOR SEQ ID :802:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

GACACAAC TGTTCACTAG CAACCTCAAA CAGACACCAT GGTGCACCTG 50
ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG 100
30 GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG 150
GACCCAGAGG TTCTTTGACT CCTTTGAGGA TCTGTCAACT TCC 193

35 (2) INFORMATION FOR SEQ ID :803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

403

(xi) SEQUENCE DESCRIPTION: SEQ ID :803:

5 AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA 50
AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC 100
AATAGCGTAC AGATTTTTC GCATTAATCC GTGTTTATAT TAACAGATTC 150
10 GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCCTCT CTCTAGATAA 200
ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTCTAAA 250
CGATAACAAG AACCCAGTA GGTAGTATAG CAGTCTTAA 290
15

(2) INFORMATION FOR SEQ ID :804:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :804:

AACCTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA 50
30 AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC 100
AACATTTCCG GCAATTTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT 150
CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCTAC CACTTCCGGG 200
35 CCCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCCACAAA 250
ACAGGG 256

40

(2) INFORMATION FOR SEQ ID :805:

(i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10	AGCAACCTCA AACAGACACC ATGGCGCACC TGACTCCTGA GGAGAAGTCT	50
	GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA GTCGGCGGGG	100
	AGGCCCTGGG CAGGCTGCTG ACCGATTTAC CCTTGGACCC AGAGATTCTT	150
15	TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG GGCAACCCTA	200
	AGACGAAGGC TCATGGCAAG AAAGTGTTCTG GTGCCTTTAG TGATGACCTG	250
20	GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC	286

(2) INFORMATION FOR SEQ ID :806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :806:

35	TTCTTCATCA GATTTTACAT CTGCCTGATT AGAATCTTCT ACACTGGCCT	50
	CAGAAGATGA TTGTTCAAAA CTTTTTCTAA GTTGCTGTAA AAAAATTCC	100
	ACGGACAAAG TAAAATGCAG TTCTTTATCG TTTAGCCAGT GTACAACAAA	150
40	AGGTCCAATC TTCTCTTCAT TTTAATTCAG ACTCAGAGAT GTAATAGATG	200
	GAAGAAGTGA AATGTCTGTG GCTGGGTGTA TGCTGGCTGC AATATGAAAG	250

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

(2) INFORMATION FOR SEQ ID :807:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :807:

15 AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTATTAG GCAGAATCCA 50
GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG 100
GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAGAAAG CGAACTTAGC 150
20 GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG 200
GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC 250
25 ACAGACCAGC ACGTCGCCCCA GGAGCC 276

(2) INFORMATION FOR SEQ ID :808:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :808:

GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT 50
40 CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA 100

406

ACATCGCTAG CTAATTTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG 150

AAGCTTGTTTTC TTACACAGTT TCCCTTCAGG TCCTTTGATG AATCATACTG 200

5 ACGTGATCGC TTATCGTA 218

(2) INFORMATION FOR SEQ ID :809:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :809:

AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA 50

20 CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT 100

TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCC 150

25 TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC 200

TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCGAAG 250

ACTAATGGCA AGCAAGTGCT AGACGC 276

30

(2) INFORMATION FOR SEQ ID :810:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC 50
CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTTCTTCT 100
5 GAGGAGGCTT ACTGCTTTTC TTA CTGATT TATTTTTCAG AGTTTCTTC 150
TTCGTACTTT TTTTAACGCA AGTATTTTGC TTTTATTCT CCTCCATT 199

(2) INFORMATION FOR SEQ ID :811:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :811:

20

AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA 50
AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC 100
25 TGGGGGGCTT GCGTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA 150
GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT 200
TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT 250
30 AAGT 254

(2) INFORMATION FOR SEQ ID :812:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

408

(xi) SEQUENCE DESCRIPTION: SEQ ID :812:

TTTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA 50
5 CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA 100
CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA 150
CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCTTTC CAAACAGGCA 200
10 ACCTGCACCG GAGGGGAGAC TTTTTCGCCA AAGCGACGGG CCAGCACACA 250
GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA 284

15 (2) INFORMATION FOR SEQ ID :813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

ATACAACAGC AGAAACAGGT ATCCACGCAC AGTCCAGCAA CATTTCTTCT 50
GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA 100
30 GGCAAGGATG CTAACCTGAA GTCAATCAGC CGAGTGATGT CATTACAAC 150
CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG 200
35 CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAAG AGCTAGACGA 250
CTGACGAAAC CTGAGAACCC CGAAGGACT 279

40 (2) INFORMATION FOR SEQ ID :814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

409

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :814:

10 AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC 50
ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA 100
CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG 150
15 GGCGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC 200
AGCAGCCA 208

(2) INFORMATION FOR SEQ ID :815:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :815:

30

AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG 50
CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAACATG GCCTCCGATG 100
35 TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC 150
AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA 192

(2) INFORMATION FOR SEQ ID :816:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs

410

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :816:

GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG 50
10 CCGCCTGGGG TAAGGTAGGC GCGCACAATG GCGAGTATGG TCGCAGAGGC 100
CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA 150
15 CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG 200
GTGCCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCAAC 250
GCGCTGTCCC CCTG 264

20

(2) INFORMATION FOR SEQ ID :817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :817:

ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA 50
35 AAAACCACTC AACAAAGCAA CAACCCATCC TGTTTTTCATA ACGTTATCGT 100
AAC AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA 150
AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA 200
40 TG 202

411

(2) INFORMATION FOR SEQ ID :818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA 50
TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA 100
CTGTATAGTT TTTTAAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC 150
CCCATAGGAT AGGTAATGAA CTTTTTGT 179

20

(2) INFORMATION FOR SEQ ID :819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAACT 50
AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAA AAGAATTTAA 100
GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT 150
CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAAGTG GATCAAGTTG 200
TACGCGGGTC CACGAAGTGA CAGACGAAA ATGAACGCAA GCTGATGTAA 250

40

412

ACGCATCACA

260

(2) INFORMATION FOR SEQ ID :820:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15 ACTCGGCACT TTCTTAGAAT AGACAATTG CAAAATGTCC ATCCCAGGTT 50
CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG 100
TGAAC TTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC 150
20 ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC 200
TTTCCGTAAC TGAGTTTGAT TTCTCC 226

25 (2) INFORMATION FOR SEQ ID :821:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

CACCTACATA TAGATGCACG AAGTACTTGC TCAC TTTTTT TGGTTGTAAA 50
TTTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA 100
40 GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC 150

413

GTGATTTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC

197

(2) INFORMATION FOR SEQ ID :822:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15 GGA CTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG 50
GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG 100
GCAATCTCAA TGGCACC GCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT 150
20 TCGCGCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT 200
CACCCCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT 250
25 AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA 300
CATG 304

(2) INFORMATION FOR SEQ ID :823:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :823:

40

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTG

50

414

GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG 100
CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG 150
5 GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG 197

(2) INFORMATION FOR SEQ ID :824:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20 AAAACAATG TCATTTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA 50
CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT 100
GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCCTGACT TACCCTGGCA 150
25 GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTCCTTA ATAGCAATGA 200
TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCCAG ACAGCAAGCG 250
30 TTTTCCACA GGTCTCGACA CACAGAAGAT A 281

(2) INFORMATION FOR SEQ ID :825:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

TATTAAATTT ACTAGAATGT TACAGTTACA AATTGGTAA TGTTCTTTCT 50
GAAAAACAGC CTAATTTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC 100
5 TTTTATTCAT GATAGAAAAA TAATTCCTGG CTCATCTCA CAATTAACTA 150
ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTTT TCAGTGATGA 200
TCAAAGTGAT TCTCCCAGGC CAAAAATCA AATAAGAAGT TATATTTTAA 250
10 AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT 300
CTACTAATTG GC 312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA 50
GGGCAGGGAG GGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA 100
30 TCCCAAAGCC CTAGAGACCC CTTCAGTGA GCACCTGCCC CCGGGTCTCA 150
GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA 189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

416

(xi) SEQUENCE DESCRIPTION: SEQ ID :827:

5 CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT 50
ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA 100
AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT 150
10 TTAGAGATTA TTTTGTTGCC TGGAAATCTG TCTCATCACA GAGTGTTAAT 200
ATACACCGGC GGGATATTCA AGAGTGGCTA AG 232

(2) INFORMATION FOR SEQ ID :828:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25

GGACATTGGA ACACTATACT CTATTATTGC GGTGCGTCCT AGCAGTCTCG 50
CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT 100
30 TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC 150
TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT 200
CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA 250
35 GTAATTACCC CATATCATAA AATGCGGGCG GG 282

(2) INFORMATION FOR SEQ ID :829:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid

417

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

	CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC	50
10	TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA	100
	AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGGCGCTT AACGTGCTCA	150
	AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTCCAGAA GTTCTGAGGC	200
15	TGGACATCGG CCCGCTCCCC ACAATGAAAT	230

(2) INFORMATION FOR SEQ ID :830:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30	TTCCGCAAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA	50
	GATCAATGAC TTTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAAATG	100
	GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA	150
35	TAAACTTAAC AAGAAATGTT GCAAAACCAT TATGTGAAAA TTACAACACT	200
	CCTGAAGACG CAGACACACC TAACAA	226

40

(2) INFORMATION FOR SEQ ID :831:

(i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10	AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTTCCTT CTTTCTACA GCCTGCAGTT CATTTAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT	200
	GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT	247

20 (2) INFORMATION FOR SEQ ID :832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

	CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112

(2) INFORMATION FOR SEQ ID :833:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid

419

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA 50

10 ATGTTTATCT CATAACTCTC CTCCCAGCAG TGCACCAGTA AACTCAGATG 100

CCTGAGTGCT TGTGGCCACC ACACAACAGA TCGGGCCTTC CTCTTCACTG 150

GCCCCCTCGGC TGCTGCTGGG TCC 173

15

(2) INFORMATION FOR SEQ ID :834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCCTT ATGACACAAT 50

30 TCCATCATTC TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTTT 100

CAGACTTATC TTATATTTTC ACTTCCCCAT ACCTGGAATC AATCACTTCT 150

CCGAGGATGC TTGATTCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC 200

35

GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG 250

AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT 288

40

(2) INFORMATION FOR SEQ ID :835:

(i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :835:

10	CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAACCAG CAAGTTTTTA	150
15	TTAGTGATTT TAAAAGGGGA GGGAGTGTAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTTACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	310

(2) INFORMATION FOR SEQ ID :836:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :836:

35

	TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTA	150
	CATCTCCCAA AATGCCTAGC ATTCTTC	177

421

(2) INFORMATION FOR SEQ ID :837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC 50
CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGACAAA 100
TGTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT 135

(2) INFORMATION FOR SEQ ID :838:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :838:

30

TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT 50
GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA 100
GAGGTAATCA AAAACTCGAG CATGTATTTC AGGATCCATG ATTGAATTAA 150
CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA 200
G 201

40

(2) INFORMATION FOR SEQ ID :839:

422

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10

TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA 50
GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA 100
TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT 150
CTGAGATGTA CACGAACGAG ATCTTTTGAG A 181

(2) INFORMATION FOR SEQ ID :840:

20

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30

CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG 50
TTTTAGTGAA CATTGAGAGG AGTTTGAAG AAAGTCGCTG CACAATCTTC 100
ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA 150
TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA 200
TAATAACATG GGTTTAAAAA AC 222

40

(2) INFORMATION FOR SEQ ID :841:

423

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10

CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCTTGCT CTTGCTGCGG 50
CTCCTATCTA CCGGCTACCT GCTGCCCGCT TTGCTCCTGC TACCGGCTCC 100
GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCTGCT CACAACTCCC 150
TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC 200
TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT 250
GTCATTGTTT TGGAATTCT CCTTCAGCTT GGTCTTTTGC CGG 293

20

(2) INFORMATION FOR SEQ ID :842:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35

ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC 50
TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTT TGGCAGGTCA 100
GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCCCAA GACACACAGG 150
AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC 200

40

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAAAAAA

239

(2) INFORMATION FOR SEQ ID :843:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15 TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTTC 50
AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA 100
CTCACTCACT CTATAATAAA ATGTTTGCAC TCAATTTATA TAGTAGTGTT 150
20 TGTC 154

(2) INFORMATION FOR SEQ ID :844:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35 GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG 50
CCAGGAGTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC 100
TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC 150
40 TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCCTCAGC CTACCCTATC 200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCCTAG CAGGTTCCCC 250
ATCTTTTCCA GGCTGCCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG 300
5 ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTTGT GAGCTGTAAG 350
GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT 392

(2) INFORMATION FOR SEQ ID :845:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20

CAAAGAATAA ATAATTTTTC TATTCCTGAA AGTAACTAA TTATTTATTA 50
GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTGAGA AAGTGATATG 100
25 AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT 150
GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA 200

(2) INFORMATION FOR SEQ ID :846:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40

TTAAAAATAC TCTGGAAAGA GCACTTCCAT CGTTCATTTA CATCATATTA 50

426

	GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG	100
	AGGAGCGAGA TCTCCCAAG CCTCCAGGAT TGCAGTCTGT TGTGCCTT	150
5	CACTCCCTAA TAGGTTTGCC TTATTTAAAG GACCCACCTT CAGAGCTGCC	200
	AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC	250
	ATTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA	300
10	GAGGAGGTGG T	311

(2) INFORMATION FOR SEQ ID :847:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 287 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

25	CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA	50
	CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC	100
	GGCAGGAACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC	150
30	CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG	200
	GCAGCTCGAG GCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG	250
35	CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT	287

(2) INFORMATION FOR SEQ ID :848:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

427

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC 50
TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA 100
10 TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG 150
AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AAATATACA 200
AACACGCAAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG 250
AGGCATATNA CCA 263

(2) INFORMATION FOR SEQ ID :849:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :849:

30

TTGTCAGTCA GAATAGGATG TAAAAGACTA TTTCAAAGAG TTAAATTATT 50
TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG 100
35 CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT 150
TGACATTAAA AACGAATGGA TACCCAATC TGAATTCCAT ATCGTTTTTT 200
AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA 250
40 GTTTATCGAA ATCCTGCCGC TACTAAACA 279

428

(2) INFORMATION FOR SEQ ID :850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC 50
AGCATCTGGA TAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT 100
GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA 150
TGTTTATGAG CTCTCGACAG AAT 173

20

(2) INFORMATION FOR SEQ ID :851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA 50
TGGAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG 100
TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG 150
GGACTACAGC AACAAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC 200
AGCAGGAATT TTCTGTAA AATATTTTGG CCGTAATACT 240

40

429

(2) INFORMATION FOR SEQ ID :852:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :852:

ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGGAATGTTA 50
15 AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACACATCT 100
GCTTATTATG AAAGTGTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC 150
CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA 200
20 TTCTCTTAT AAAACAAGGG CAATTTTGTG AGAGCTACTG ACGATTTTCC 250
CCTCGAAATT TACTATTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG 300
25 TCCTTGCCGT CACT 314

(2) INFORMATION FOR SEQ ID :853:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :853:

TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA 50
40 CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTGGT 100

430

ATTTCTTCAG TGACAAGCAA ACTATCCCCC CACATGCCTT TAATGGCCAG 150
TGTTTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA 200
5 CTGATACGCT AACCTTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC 250
GCGCCAATAC TGCTTAA 267

(2) INFORMATION FOR SEQ ID :854:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC TTTCTTTTTT TCCAAAGGAA ATTCATATA GAGTCCATTC 50
ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG 100
25 GCTTGGAGCC CCCAGCCTCT TTGCTTTCTC TTATCCCTAT AGGATGGCCA 150
TTAGGTGAAG CAGTTTAGCT TGTGGTTCA GACCTG 186

(2) INFORMATION FOR SEQ ID :855:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTTGA AAA GAAACCTACA AAAATTGTAT TTCCATATTT CATAGTCAGC 50

431

CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGTTCTGC AAAAATTGCG 100

GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT 150

5 GGCCCAAAAA TT 162

(2) INFORMATION FOR SEQ ID :856:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :856:

TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA 50

20 GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT 100

GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG 150

25 GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC 200

AACATAACAA ACCCAATCGC CCTGTAACT TTAAATCTTC AACTCGAGAA 250

AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC 286

30

(2) INFORMATION FOR SEQ ID :857:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

AACTATATGG TATTATTCA CGCTGTACCC AGTCCATTGC TTGAACTTAC 50
GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTTT 100
5 CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG 150
ATTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC 200
TTTTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTTCT GTTACTTAAT 250
10 CGGCGCCAAG GCCTTTACAT GAATACTCAG 280

(2) INFORMATION FOR SEQ ID :858:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25 CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG 50
GCCAGGCTGG TCTTGAATC CCAGCCAACC TCAAAGTGCT GGGATTACAG 100
CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAAA AACACAAGTC 150
30 CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTTACAT 200
CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT 250
35 TATACAGGGC TTGAACTGTC TTTTAAGCAA GCCCCAAATC CTTTGAAAGG 300
AGGCAGTAAC 310

(2) INFORMATION FOR SEQ ID :859:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs

433

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

10 TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG 50
CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT 100
CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC 150
15 AGGAAGAG 158

(2) INFORMATION FOR SEQ ID :860:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

30 TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT 50
CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA 100
TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC 150
35 AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT 200
TAGATTGCGA ATAAGTTGAA AATAAATCCC AACCACGTAA CTTACTAAAG 250
GAATAATGAG CCA 263

40

(2) INFORMATION FOR SEQ ID :861:

434

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10 ATTTGCTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG 50
GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAAAGT ATAAAAGATT 100
15 ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGTTT 150
TGATCCCATTA GGTCAATTGT TATTACTCTT CTTCAACAGA GTGATTTTCT 200
ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG 250
20 AAAG 254

(2) INFORMATION FOR SEQ ID :862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35 GTTCCTCCTT TGTAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT 50
GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC 100
CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGTCTGC 150
40 TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA 200

435

	TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC	250
	TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT	300
5	TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC	337

(2) INFORMATION FOR SEQ ID :863:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 10 | (A) LENGTH: 169 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :863:

	TGGTGGGTTT GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC	50
20	GGTGGGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC	100
	TCTCAGCGAC GAGGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA	150
25	ACTTACAATG CCACCGCGA	169

(2) INFORMATION FOR SEQ ID :864:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 30 | (A) LENGTH: 286 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :864:

	ATTAAGGTAA AGGAAGACTT TCCATTGTTA AGTAGAAGA GTGTCCTGCT	50
40	ATTACTACCA TTCACATCTA GTTTGTGTGA ACTAGGGTTT TCTATCTTAA	100

436

CCCTGTAAA AACAAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG 150
CGGATAGCAT TATCTTCCTG TGTCCAGAC TGAATGAAT TTATGAACAA 200
5 GGCAAGCACA CCATTATAGT AAATAAAATC TTACCTAGTT TTCGTTTTTG 250
CATTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC 286

(2) INFORMATION FOR SEQ ID :865:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20

ATATAGTCCG CTAGGGATAG TGAAAAATTT GGGGCTTGGT TTAGATTGGA 50
GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG 100
25 GCCTTGATTT CTGTCCCCCT TGCCTTGCGT GGCCTTTGAA TTGAAAGCTT 150
TGAATTAGGC CTTCATAGAT TTAGTGTGC ATACAAATAA CACGATCTTT 200
TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC 250
30 GCATTCTGA TCTATAAGGT GA 272

(2) INFORMATION FOR SEQ ID :866:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

437

(xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAAACTAAGT CAAAAAACG GAACGCAAAT 50
5 AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG 100
GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG 150
CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG 200
10 TTTCTAACAC TACAACGCTA ACTTTTGGAA CGTATCTACT TCTAGCATGT 250
AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG 296

(2) INFORMATION FOR SEQ ID :867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG 50
CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA 100
30 CTGTGACTTC TACGATGAAA GAACAAGGGA GACAAGATCT TATCGACAAT 150
CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT 200
35 GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A 241

(2) INFORMATION FOR SEQ ID :868:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC 50
ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT 100
CAAAGCCCAA TATAACCAAG GGAAGGAAT 130

(2) INFORMATION FOR SEQ ID :869:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :869:

TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTTGAAAAA 50
CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATTT TGAAATTTAA 100
TTCAAATGGT CAAATTCCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT 150
TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA 200
TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT 250
TCCCAAGCAC TTAAACAATA AACAAATGCC TCTTTATACA AACCTTTCCC 300
AGTAATAGAA 310

(2) INFORMATION FOR SEQ ID :870:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs

439

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :870:

10	AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA	50
	TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC	100
	CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG	150
15	CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG	192

(2) INFORMATION FOR SEQ ID :871:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 250 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :871:

30	ACCATAGATG TGTTCCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG	50
	AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCAGAT CTTTCTACAT	100
	TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA	150
35	CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTCATGGAG ATTTGAATAA	200
	TCTATCCGAT GAGATTTATA TNTAACAAC TCAACTCCTG TCGAAACAAA	250

(2) INFORMATION FOR SEQ ID :872:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs

440

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :872:

10	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
	AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG AACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
	TTCGTGGCCA GGGAAACACA TGTCCAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313

(2) INFORMATION FOR SEQ ID :873:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC	100
	ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT	200

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAAACT 250

ATCCAGCGTT AGCACAAATG 270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTT ATCTCCAAAG CCAGCCATGG TGTATTTCTC 50

TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT 100

20 GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT 150

TAATGACAGC TGATTATTTT CATCTGCAAA CTTACTCAAG AATGCAATCC 200

25 AGACTAACAC GACAATAGGA CATCAAGCT 229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 294 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAACTTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC 50

40 CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT 100

442

TGGTCTTGAC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG 150
AAGGCTTTTG TGTTCCTCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA 200
5 AGCACCCTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT 250
ACACGGAACT GTCCTCGACC CGTGGGTAAC AGTATTTTCT GCGT 294

(2) INFORMATION FOR SEQ ID :876:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :876:

20

ATTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG 50
TAACTAACAT GAAACCACAG AACTGTAACT CTGCCACAGC TGCATGAACT 100
25 CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT 150
ACGCCAACAA AAACCGTTAT TAA 173

(2) INFORMATION FOR SEQ ID :877:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :877:

40

TAATCAAAAG AGCTCTAAAT CTGTAATTTC TTTCTCCTTT AAAAAAATGT 50

443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG 100

AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTTCG AAC 143

5 (2) INFORMATION FOR SEQ ID :878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTTTCAG TGGTTCCTGC TGTGGGACTT 50

GCGTTTTCAC TAAGTGTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC 100

20 AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA 150

GGGCTTCTAT TGCTAATGCC TGTAAACCTT GCTGAATCTA TAACAGAGTC 200

25 TATACCGCTC TCG 213

(2) INFORMATION FOR SEQ ID :879:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA 50

40 ACGAGATAGA CACATGCTTA TTCAAACCAC AGATATGATC CAGTTAATTC 100

444

CCTTCTTAGA ATGTGCCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT 150
AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC 200
5 TACCAGAGTA ACCGTCATCC CCTTGAG 227

(2) INFORMATION FOR SEQ ID :880:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :880:

ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG 50
20 AAGCCTCAGG AATTCCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT 100
TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA 150
25 TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA 200
ATAATCACTC TTTACAAGGT A 221

(2) INFORMATION FOR SEQ ID :881:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:

40 AATTGTGGTA TATTTCAATT AAAATCGATC AAAGACAGCA ACATACATTA 50

445

ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT 100
CATATTAAAA CAATGATAAG TAATACTTAG AAAGTGCATC CTAGAGACAC 150
5 ATCATTGCGA TTTTGTAGAA AACAGAAACA TATTAGTGTG AAAAGATGTT 200
AAAAAATGAA TATTAAACCG TCGAGCAGAA CACACTACGC CGATAACAAT 250
ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT 300
10 GGCGATCCGA 310

(2) INFORMATION FOR SEQ ID :882:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25 GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT 50
GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA 100
CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA 150
30 CGAACTACAA ACGTAACAGC AGCAGGC 177

(2) INFORMATION FOR SEQ ID :883:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCCTCTGA AGATACACGT 50
5 ATAAACGCCA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150
GA 152

10

(2) INFORMATION FOR SEQ ID :884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50
25 GACCTATTTT AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT 100
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150
AAATGAAATT GTGCCGAAAT GTATACA 177

30

(2) INFORMATION FOR SEQ ID :885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

5 CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT 50
TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAAGTAGAA 100
TTTTTTTATA TCCACACTCT AGTATGAAAT GACTACTTAT AGAGTAGAGT 150
GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTA CAAATATATA 200
TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A 241

(2) INFORMATION FOR SEQ ID :886:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

GTAGCAACCG GCGCTCAATA AAATCAACC AGCAAACG ACAAGTAACA 50
25 ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA 100
ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG 150
CCATCCATAT ACCAAAAATG CTAATTACAA CACCACAACA 190

30

(2) INFORMATION FOR SEQ ID :887:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA 50
CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA 100
5 CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA 150
CTATAATATT ATACTCTC 168

(2) INFORMATION FOR SEQ ID :888:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20

ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT 50
GCCGATCTCG CAACCGGTTT CAGTTAGACA GAACATTGTG ATATTCAAAC 100
25 CACTTTCTCG TAATTTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT 150
AATCATATTC TAGTCCACTG TAGC 174

(2) INFORMATION FOR SEQ ID :889:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40

ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA 50

449

	TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA	100
	TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT	150
5	ATATGTGTGT GTACAATATA TAAAAAATTA TATGGGAGAA AAGAAAGGCA	200
	AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTTG TGTGTAACAA	250
	AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT	300
10	ATATATATAT CTGTATATAC AGGTATA	327

(2) INFORMATION FOR SEQ ID :890:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 181 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25	TTTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC	50
	GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC	100
	TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT	150
30	ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T	181

(2) INFORMATION FOR SEQ ID :891:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 207 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
40	

450

(xi) SEQUENCE DESCRIPTION: SEQ ID :891:

	CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCTCAC	50
5	TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT	100
	TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTTT GGCAACCCAA	150
	TTCACAGTTT TGTAATTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG	200
10	CAAAGAA	207

(2) INFORMATION FOR SEQ ID :892:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :892:

25	CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG	50
	TGATTTTACA GTAGAGTGAA CGAACTTGG GAAGGAAAAC ATCCAAGAGG	100
	CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT	150
30	TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAAACACTC TCTACTCT	198

(2) INFORMATION FOR SEQ ID :893:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 96 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

451

(xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT 50
5 TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG 96

(2) INFORMATION FOR SEQ ID :894:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :894:

AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA 50
20 ATGGAAACAG CATAATACTA CATACTATCG CGCGGGGTG TCGGCGTGGT 100
GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA 150
25 GAGTGAGCGT GGGAGGGTGT GGTGGGTGGA GGTGTGTGGA GAGGTGAGTG 200
TGCAGAGAGG GCGAGTGTAT GTGTGATAAG TATAGCGCGC AAGAGGCGAG 250
GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAAC 300
30 AATAACCACT ACTCACATAG AATAT 325

(2) INFORMATION FOR SEQ ID :895:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

5 ATAGTTGTAC ATTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC 50
 AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA 100
 TTTATCATTT ATTGTGTTG GAAACATTCA AACCTTTTCT TCTAGCTATT 150
 TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTGTGAAT 200
10 AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTTGAT ATACTGATTT 250
 TCTTTCTTTT GTTATA 266

15 (2) INFORMATION FOR SEQ ID :896:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 197 base pairs
 (B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

 AAGAAGAGTC TTCTGCACAA ACAAACCAT AGTGTGACA AATAGTCATG 50
 GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG 100
30 GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAAACT 150
 AGCAGGCCCA GAAGACCGCC CCGCCCCCA TGCCCTGGCG CAGGGCC 197

35 (2) INFORMATION FOR SEQ ID :897:

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

453

(xi) SEQUENCE DESCRIPTION: SEQ ID :897:

5 GATGGCTGGA GTAGATTAGG GCGTAGGTAG AACTAGAGGT TAAGGAGGGT 50
GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTGTGAA 100
TATTTTCTT CCGACTAACT CGCGCCCCAC TCTCTGCGA GCACAAACAC 150
10 ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT 192

(2) INFORMATION FOR SEQ ID :898:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :898:

25 TGGATGTTTT CATTGCAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC 50
TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG 100
AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT 150
30 ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT 200
GCTCTAGTAG CCCACAGCCC AATC 224

(2) INFORMATION FOR SEQ ID :899:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

454

(xi) SEQUENCE DESCRIPTION: SEQ ID :899:

	GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG	50
5	TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA	100
	AATGCAAAAT ATTCTAATGT TTCAATGTTC TACATGAACA TATAGGGAAG	150
	CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC	200
10	CGAGTCTGGC TACTTTCTAG GTAGTGTGCT TTTGTCAAA TTATAAGAT	250
	ATATTCCCTT TGTTTTTTGA AAACGAGTGA GATGCTTAAA TAGAGTACAA	300
15	TTATCTCATT CAAAATGTAT GTTGTTCCT CTCGAGAATT GTGAAGGTTT	350
	TGAGATTTGA TT	362

(2) INFORMATION FOR SEQ ID :900:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30

	GTATGTAGCC CAGTGGGTGT CTTCCACAG GGTAGGTACT CAGTTTGCTC	50
	TGGAGGGTGA CTCATACCTA AACAAGTGCA CATCTCCTTT CTCAGTAAAG	100
35	CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT	150
	ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA	200
	AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA	250
40	AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTTCTGTC AAGTTTGGT	300

455

TTCTCGATGA

310

(2) INFORMATION FOR SEQ ID :901:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15 TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA 50
CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGACTCCTCC AAAGATTGCA 100
GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC 150
20 CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA 185

(2) INFORMATION FOR SEQ ID :902:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35 ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG 50
TCAAACAACCT AAACCTACTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA 100
GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA 150
40 CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTTACTT TTTAGACTAC 200

456

AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAACCTCTG TAAAGAGTAA 250
GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT 300
5 TGCCTTCAGA AACACTTTGC CTTTAAATAT GTGTAGCTAC AGTAAGTACC 350
AATGGGCTAA CTAATTGAAG CTAACATTTT A 381

(2) INFORMATION FOR SEQ ID :903:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAACTG ACATATGTAT 50
ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC 100
25 CTCTGCGCTG TTGCGGGTCC TGC GGAAGTC CTCGGAGCGG CCGTCGCGGA 150
AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC 200
ACTTTTTTTT TATCGGCACC AGGCCGCGTC CTCCTCCTCC 240

30

(2) INFORMATION FOR SEQ ID :904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG 50
TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTATGGGC AACCCTAAGG 100
5 TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG 150
CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA 200
CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTCAGGCTC CTGGGCAACG 250
10 TGTGGTCTG TGTGCTGGCC CATCACTTTG 280

(2) INFORMATION FOR SEQ ID :905:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25 GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT 50
AAAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT 100
ATTGACACGA GTAAAGCGTA GCAAGTTTAA CACAACTTAT GTAAACTTGG 150
30 AAAATTTTCC GAAATTTTAT TGACTTTTCT CGGTCTCTCC TATCTTTATA 200
TACACATCTC TCATGCACAC ACGCG 225

35 (2) INFORMATION FOR SEQ ID :906:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

458

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

5 GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA 50
ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA 100
TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG 150
10 TCCACTGTAG C 161

(2) INFORMATION FOR SEQ ID :907:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :907:

AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAT 50
25 ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT 100
TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT 150
30 TATATATGCG CACACACACA CACACACGAC ACGACGACAC ACACACACAC 200
TCTA 204

(2) INFORMATION FOR SEQ ID :908:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

459

(xi) SEQUENCE DESCRIPTION: SEQ ID :908:

	AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA	50
5	AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC	100
	TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC	150
10	ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA	200
	CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA	250
	CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC	300
15	CAAATGTGTG TGTTTT	316

(2) INFORMATION FOR SEQ ID :909:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 20 | (A) LENGTH: 307 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :909:

30	CTAGTAACAT AGAAAATAAA CTTCACTGGG AATCTCTGCT TCCCGCGTGA	50
	GGTGTTTAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT	100
	CAAGTTAGAG GAGATGGCAG GGTCAAATTT TTAGAACTG GATCCCACCA	150
35	CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA	200
	TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCAG	250
40	GGAAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTTAA	300
	GCTATTT	307

460

(2) INFORMATION FOR SEQ ID :910:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTTGCTC AATCAAACGC 50
15 AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT 100
TAAACCGAAT CCCCAACAATC TCAAACCTCAA CCAGGCCAAA GGGAACACAG 150
TGACACAACA ACAGGGTTCC AA 172

20

(2) INFORMATION FOR SEQ ID :911:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA 50
35 CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG 100
AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAGAG 150
AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA 200
40 TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG 250

461

CATCT

255

(2) INFORMATION FOR SEQ ID :912:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15 CAAGCGAATG GTAATTACAT GGTCCGATGA GGTCCCTCACT CTCAGGGGAG 50

GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACTACTGTTT 100

GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT 150

20

GCAATTTACA AGAGATTTCT TTGAAAGAAA ATAGGAAGGC AAAGAA 196

(2) INFORMATION FOR SEQ ID :913:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35 ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA 50

GCGATTTTAC AGTAGAGTGA ACGAACTNG AGAAGGAAAA CATCCAAGAG 100

GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA 150

40

TCCCCTAGG GCCACGAGAA ACAAAGCAAA TTAAACATT ATCCACTACA 200

462

CGA

203

(2) INFORMATION FOR SEQ ID :914:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15 CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA 50
GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT 100
AGCCTGGCTC TGCCCCGAG AACGGTCTGT GTGCTGTTT AAAATAAATC 150
20 TTAGTGTTCA AAACAAAATG AAACAAAAA AAAATGATAA AAAATCGGA 200
TTTCCGGTTA AACTGTGAC TTCAATTGAA ACACCTTTT GTAGTATCTG 250
25 GAGGTGGACA TT 262

(2) INFORMATION FOR SEQ ID :915:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :915:

40 TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT 50
ACACGGAGTC TGTATTTTGC ATCCTAGAAT GATTAACCAG AAACAAAGAA 100

463

AGGAAAAAGG TAAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT 150

AAAGAATGAA ATAATTTGAA AAAAAAGGCA GGGCAGGCAA A 191

5 (2) INFORMATION FOR SEQ ID :916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT 50

TCCAGGAGTT GTCCTTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTGT 100

20 GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC 150

AGTGTGTGCA TATGTTTGTG TGGTTGTCTC TGAGTGATAT CCACCTCTCT 200

25 CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG 250

TG 252

(2) INFORMATION FOR SEQ ID :917:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :917:

40

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA 50

464

GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT 100
TCCTGAAGGT CATGCGATCC TTTACCCTCA GAAACTTTCA GGCTGAAATC 150
5 ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT 200
CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC 247

(2) INFORMATION FOR SEQ ID :918:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

ATTTGGATTC AATTGCCTGT TGCACITTTA CATTAACTGT TGCTTAAATA 50
AACAAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG 100
25 CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT 150
TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T 191

(2) INFORMATION FOR SEQ ID :919:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAGAA 50

465

ACAACCTCCT CATTTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG 100
ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT 150
5 CGAACAAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC 200
AACCC 205

(2) INFORMATION FOR SEQ ID :920:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTCCTC TCCAACGACT 50
CGTTCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA 100
25 CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACCGCGTT TAAGAGATGA 150
AACCACGACT TCGTCAAGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT 200
TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA 250
30 AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG 300
CTCTAAGCTA CAGGTTGATC ATA 323

35

(2) INFORMATION FOR SEQ ID :921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

466

(xi) SEQUENCE DESCRIPTION: SEQ ID :921:

5 AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA 50
GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG 100
ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG 150
10 GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCGGCGG GGATCAAAAC 200
TATAGAAACA ACAAGTTAGA GTACAGACGT 230

(2) INFORMATION FOR SEQ ID :922:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25

TATTTTTCCT GATGTTCTCC CTCCTCCAG TCCCCGACCT CCCACAGGCC 50
CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTTCA 100
30 TGCCCATTTCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCTCGCTC 150
TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC 200
TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTGTAA 239

35

(2) INFORMATION FOR SEQ ID :923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

467

(xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5	GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT	50
	TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT	100
	TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC	150
10	TGAAACCCGT CCACTCAATA AATTTTGT	178

(2) INFORMATION FOR SEQ ID :924:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 325 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25	CAGCTGGTCC CCCACTAAAA GAAGGGGCGAG ACCACCACTA GCCAAAAGAG	50
	ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC	100
	AAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT	150
30	TCTTGCTTCT TGTTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA	200
	GCAATCTCAT GGTTCCTTGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA	250
35	GTAATCAGAG AGAAGATAC CAAGGAATGC TTTTCTGGC CTATTCATTT	300
	ATTTTGGGG GATGAATTTA CACTA	325

(2) INFORMATION FOR SEQ ID :925:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 261 base pairs

468

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :925:

ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG 50
10 AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT 100
CCGGTTTTCT TTGTTTTTTC TCTTTATTCTG TCCTTTCTCA AAGATGGGAT 150
15 ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG 200
AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG 250
TTCCAGTCCT G 261

20

(2) INFORMATION FOR SEQ ID :926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :926:

GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC 50
35 AACTGGGTTC AAATCCTGGC TCTGTCACAT ACTAGCTGTG TGACCTTGGC 100
CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT 150
AACCAACCAA GAGAGCTGAG AGA 173

40

(2) INFORMATION FOR SEQ ID :927:

469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10

AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC 50

CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TGCGCCATCC 100

15 TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC 150

CTTNGATTTT TCTGCCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCAGC 200

TCAGATCATT ACTACTGAAC TCG 223

20

(2) INFORMATION FOR SEQ ID :928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :928:

GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT 50

35 ATTTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA 100

CCACAGATTA AGTGAAGACA CCCACAATT TAATGACTCT ACGACTCTCG 150

GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT 200

40

CATAACTTGC AT 212

470

(2) INFORMATION FOR SEQ ID :929:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :929:

TTAACATAAT ATTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT 50
15 ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT 100
TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG 150
TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG 200
20 ACATAACTTG AGTTTGTGTTG CTTGGTATTT ATT 233

(2) INFORMATION FOR SEQ ID :930:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35 AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA 50
GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTCAGCACA TTCATGGTTC 100
AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA 150
40 GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC 200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

(2) INFORMATION FOR SEQ ID :931:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15 CTATCTAGAA TTACTTATTT CACTTGAAAT GTATGGTTTC AGGAAAATTT 50
TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGA ATAATGGCAT 100
CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA 150
20 AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC 200
ACACACACAC ACAAAAAACA C 221

25 (2) INFORMATION FOR SEQ ID :932:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :932:

TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG 50
CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC 100
40 TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA 150

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG 200
GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA 250
5 ACGGAGCAGG TCAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT 300
TGTAATTAGC CACTGCACTC CAGCCCTGAG CAA 333

(2) INFORMATION FOR SEQ ID :933:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20

AGATTTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA 50
GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT 100
25 TGTTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTCTG AATGTTTAAG 150
AAAAAATAA TACTTTTCAG AATTACCTAC CTCTTCTCA TTTTTCAGCT 200
GGGATCAATT ATTCCCTTTC AACTTTTTTT ACATCCTAAG TAGAAATAAA 250
30 ACTCTTTATT CTATTTTTTT TCACTTATTG G 281

(2) INFORMATION FOR SEQ ID :934:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

473

(xi) SEQUENCE DESCRIPTION: SEQ ID :934:

AATCTTGAT TATGTTAATA TAAAATCTA ATAATAAGAT ACTGTAGAAG 50
5 TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG 100
TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAAACTGTT 150
GTTTTATCCC AAGGGTAGAG GGA CTCTAAG TAAAACTGTA ACAGAATCAA 200
10 AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGAACT 250
TTAAATAAGT AAATCT 266

15 (2) INFORMATION FOR SEQ ID :935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAAGT 50
ACTAATAACT CATTAAATAA ATTAATAATA TTAAATGATC TGTGTGTTCC 100
30 ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA 150
TTACTCTAAC ACCAATAACA ACACGTAA 178

35 (2) INFORMATION FOR SEQ ID :936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

474

(xi) SEQUENCE DESCRIPTION: SEQ ID :936:

5 ACTCAGCTCC GTGCGACCCA CATGGCCCCA GGCGGGGGGA CACCAGAGGC 50
 TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCC ACAGCAACTT 100
 TCCCAGCCAA TGCCACGATG GAGATGACAA CCCCAGATCT GGGGANACAG 150
10 AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG 200
 ACTTCACCCG AATTACATTT ACCA 224

(2) INFORMATION FOR SEQ ID :937:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25

 ATTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAATTGCT 50
 GGGGATGGGT AGAGAAAACC CATTTATAGT ACTTTTCTGC CTTCTTGTGG 100
30 TTTTCGGCTT TGCGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA 150
 AAAACAAACA CAAAACATT TCAAAGAGA AAGGAAAAAA CTTTTTCCAA 200
 CCAAACTCC TAAAAACCC AAAACAGAA CAACCAATTA AACCCGACCC 250
35 GACACAATA CCAATGACTG 270

(2) INFORMATION FOR SEQ ID :938:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
(B) TYPE: nucleic acid

475

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA	150
15	CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
	CTAGAACTAA AGTCA	215

(2) INFORMATION FOR SEQ ID :939:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

30	TGTCGTCCTT AATATTTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTTGTC TATGTTTCTA TATCTCTCTC	100
35	TTTTACGCTT CTTTCCCGGA CCGTCCCTC CCTCTACAAT TATATTTACT	150
	ACCTTCATGA TTGCTTTTTA TTATTTCTTT CACTCATCAT TATTGTTTAT	200
	TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TGCCTTTTCT CAACCCCCCT CCTTCCTCAT	300
	TAC	303

476

(2) INFORMATION FOR SEQ ID :940:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :940:

ACACTATTTT CAAAATCCA AATAAAGTG CAGTTTCAGA CTTTTTAAAA 50
15 AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG 100
CGTTTGATG CAACACTGCA TATTTTTTCT AATCAGATTA ATATGAGTTT 150
TAATGTTTAG CATGAACTAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT 200
20 CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT 250
TGCTTTGCTT TGTGGAGACT TGC GCGTATT TTCTTTTGCT TGTTTGTTTA 300
25 TCGCCAGGCA GCGCTGTTG AACTGTGAGA 330

(2) INFORMATION FOR SEQ ID :941:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :941:

TTTATTTTCAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT 50
40 TTTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT 100

477

TTTTGCT

107

(2) INFORMATION FOR SEQ ID :942:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15 CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTTGT GTGTGTATGT 50
GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGTTAT 100
TTCGGCGTTA CACCTCCGGT GTTCTC 126

(2) INFORMATION FOR SEQ ID :943:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA 50
35 AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA 100
GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA 150
AGCTC 155

(2) INFORMATION FOR SEQ ID :944:

478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT 50
TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG 100
GGGGGGGGTT TGGAAGCAAA CACATTGGG GTTTTAAACC AATTGTTAGG 150
TTCTTTTAT TTAGGGTTGT GCAGGGAAC TTTGGGAGGT TTCTTTAGGT 200
GGGATGGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT 250
TATTTTGTCC CTTAACTTGG TTTGTTGGGC AGGTGGG 287

20

(2) INFORMATION FOR SEQ ID :945:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :945:

35

ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG 50
TCCAATTATA ATCCGAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG 100
GATCATGGGC ATGGAATTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT 149

40

(2) INFORMATION FOR SEQ ID :946:

479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :946:

10

TTTAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTAAATA 50
AATTTACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG 100
AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC 150
ATTAACATTG GAAAACCTCA GACCTGGACA CCAGAACCTC AAATCTGTGA 200
GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTTT 250
TTTTTTTCCC C 261

20

(2) INFORMATION FOR SEQ ID :947:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35

CTTTAGGAAC TGTCAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACCTG 50
CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAAAGTTG CACTATTGCA 100
AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG 150
TCCTGTACCA GAAACATTTT CTTTATTGT TACTTGCTTT TTACACTTTG 200

40

480

TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC 250

CAAGTTGTAT ATTT 264

5 (2) INFORMATION FOR SEQ ID :948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTTGA 50

GCCAGGTTGA TTGAGCACTG GGCTCCAACT TATTGTTAAT GAGAAACGGC 100

20 CCAACTTGGA CCATGACTTT CCCATTGCA GGTCTTAGAA TAATTTTTT 149

(2) INFORMATION FOR SEQ ID :949:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA 50

GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA 100

GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG 150

40 TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTG GCACCTTCCC 200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15 ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG 50
CACTGACAGA TTTACAGACA GGAAAACAAA GCCTTACTTA CCAGGAATCC 100
AAAGTTTATA CATGAAAATT TAAAAAGGGA GTCTATGCAA AGCGGAGTTC 150
20 AGG 153

(2) INFORMATION FOR SEQ ID :951:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35 TCGGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG 50
TTGTTCTTAA GGCGAGCTCA GGGAGGATAC AGAAAACCTCT CCTGTGGTGC 100
TATGAAATGT GCGGTAAAAA GCATTCTG 128

40

(2) INFORMATION FOR SEQ ID :952:

482

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10 GTTGGAATT TCCCTAAAT CACCTACCGA TTACCCTTGA TTTCCCTTGT 50
TTTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC 100
15 ATATAAAAAT AAAGTGTAAC CAAATATTGT AATGTATATT GCTGCTCTTC 150
TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC 200
AATTGATACA AAT 213

20

(2) INFORMATION FOR SEQ ID :953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :953:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50
35 TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100
TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAAGTACTAC 150
CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT 200
40 GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT 236

483

(2) INFORMATION FOR SEQ ID :954:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :954:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50
15 TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100
TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAC 150
CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT 200
20 GCCACTGCAG AAAGTGT 217

(2) INFORMATION FOR SEQ ID :955:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35 AGCAGCGACC GCGCTCACTG GCTTTTGTG TCTGCTTGGG CCTTTTCTGT 50
TCAGTCCATG CTTGAACTAC TCCACCCCT TAAATCCAAC GTAAAAACCA 100
GTCTTTTCTG TGCTTGTCT CTGTGCGTTA ATGCTTTTTC TTATGCTTGC 150
40 TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG 200

484

TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA 250
TGCTTG 256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTTCTC 50
ATTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTTATT 100
20 AATTTTAA AATAACATTA AAAAATTTTT TAAAATGTGA ATATACCACA 150
ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA 194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50
ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT 100
40 CATTTGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCG TGTGTGTGAG 150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA 196

(2) INFORMATION FOR SEQ ID :958:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15 GCGCTCAGCT GGAAC TTCG ATCTATTTTT TCTGGTCTC ATACTCAGTT 50
TTTTTATGTA GTCACCTAGT AAAATAAACC TAAAAAATAA CATTGATTTT 100
TTCTG 105

20

(2) INFORMATION FOR SEQ ID :959:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :959:

GACAGCGACC GACACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA 50
35 GCTCTATTTA TACAGCAAAT TCAATACAG TAGCTTGCTA AGCAACTTCA 100
TAATTCATTA AACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT 150
TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC 200
40 TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG 250

486

CTTTTGTAA A

261

(2) INFORMATION FOR SEQ ID :960:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15	CACAGTTTG TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA	50
	TCGTTTCTTC TTTAGAGGAG TAGGTTTAA CCATGTAAA TTTCCAAGAA	100
	TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTTC AAAAAATAAA	150
20	TAATTTTCGA TTCAAGTACT ATACAACTT AACGATGG	188

(2) INFORMATION FOR SEQ ID :961:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35	ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC	50
	TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA	100
	CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTCT	150
40	ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C	191

487

(2) INFORMATION FOR SEQ ID :962:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT 50
ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA 100
TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC 150
CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAT T 191

20

(2) INFORMATION FOR SEQ ID :963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCAGC AGGAACAGCA GCCCAATGCC 50
TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTACTTGA 100
GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC 150
CGAACACCAT CAATAACCGA ATAGACTA 178

40

(2) INFORMATION FOR SEQ ID :964:

488

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10

ACTTTCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG 50
GGGATCCTTT TGAATGCCAG ACGCGGGAAG GAAAGAATGA AATTAAAGAA 100
TATCCTTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT 150
CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC 199

15

(2) INFORMATION FOR SEQ ID :965:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :965:

30

ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGTATTTT 50
GGCACATCTG CCAAAGCTA CAAACAACCC CTAATAATTA CACACTACAG 100
ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT 150
CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTTCTCC TCGCCTTTAA 200
ACCTGCAGGT TGGGGCT 217

35

40

(2) INFORMATION FOR SEQ ID :966:

489

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTTCC 50

AATTTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT 100

15 CAAGAAAAAG CAAATGGTTT AAGTTTTTAC ATAGGAAATC TAAGAACTAC 150

TCATCAATAA AACGCAACAC TATCA 175

(2) INFORMATION FOR SEQ ID :967:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG 50

GGGGACAAGG AAAACCTGGC GGGGGGACCC GCGAAAAACA CA 92

35 (2) INFORMATION FOR SEQ ID :968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

490

(xi) SEQUENCE DESCRIPTION: SEQ ID :968:

5 GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA 50
 TATTGTTT CAG CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT 100
 ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AACTCGAAC 150
10 AAATAACCGA AACTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA 200
 CTACTAAC 208

(2) INFORMATION FOR SEQ ID :969:

15

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25

 AGTGGTTGGT GTTTACTGGA ATCTTGTTTT TTTTTTTTCG GTTTTTTTGA 50
 CTACTCGGGG GGTTCCTT TTTTACAGGA ACTAAATCAA CAACTTTTT 100
30 CGATTCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC 150
 TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC 200
 CACCAAGGAT TTAATCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT 250
35 TTAAGA 256

(2) INFORMATION FOR SEQ ID :970:

40

(i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid

491

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA 50
AATAACCTAA CCCGCTTGTT TTTTCCACAC TAATACTAGG GCGAATTCCT 100
CATTTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG 150
ACCTAAGACA TCAGATGAAA AACAATGCCT CTATTCCTTC AAGTATAATA 200
AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA 240

(2) INFORMATION FOR SEQ ID :971:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50
ATAACCTAAT CCGCTTGTT TCTCCACACT AATCCGAGGG TGAATTCCTA 100
ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TGC GCGAGGC 150
CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT 184

(2) INFORMATION FOR SEQ ID :972:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

492

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :972:

	GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA	50
10	TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTACTTGTTA	100
	CATAATCCAG TGAAAACTCT ACTTGTGAA ATTATGACAT AAAGATCTTG	150
	CAGCTTTATT TGAGTATTTG TTCTTTTGTG TAGTTTCCAT CTTTAAAT	200
15	ATTTAAATA TTTTCAAGGA TAAAGTATT ATCT	234

(2) INFORMATION FOR SEQ ID :973:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :973:

30	TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC	50
	TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA	100
	AAAAAAACAT CACAAACTG AACTGCCGCC ATCACCCTA CACCAAGTAT	150
35	GTGATTGAAT TATTCAATGA TCTGTTTTCG CGGTAGTGAC CAACANC	197

(2) INFORMATION FOR SEQ ID :974:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid

493

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

	AGCAGGAGAT TTTTSTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG	50
10	ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGACT TAAAAAATA	100
	ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC	150
	ATACAGAAAA AAACGAAATA CATAACCCCC CAGGTTTGAA AGAAAATAAT	200
15	TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC	244

(2) INFORMATION FOR SEQ ID :975:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

30	TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG	50
	AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG	100
	AGACCCATTA GAGATTTTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC	150
35	ACCTTACTAT ACACATAATA TAGAATCTGA GGAAGTACGT AACTGATACA	200
	TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT	250
40	TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA	300
	ATGTGCAATG AAGGGTTTCG TGTAATATTG	330

494

(2) INFORMATION FOR SEQ ID :976:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :976:

TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT 50
TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT 100
TCCTTACGGC ATTCAATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT 150
AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTTATAT GAATNACTTA 200

20

(2) INFORMATION FOR SEQ ID :977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :977:

AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT 50
ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT 100
AATGATGTTA TGAAACGAGC TTTGCT GCTCTTGATT GGAGCTTCCG 150
GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAG AACTGTGTTT 200
AATACTCTGA ATTTTAATTA GAAAAAATA CAATAGCAGC AAGGCCCTGG 250

40

495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC

296

(2) INFORMATION FOR SEQ ID :978:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15 GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG 50
ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT 100
AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGAAGC CGGGGGAGGA 150
20 CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC 200
CAGCCACTAC TGATAATTCA CAACGGTA 228

25 (2) INFORMATION FOR SEQ ID :979:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :979:

CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT 50
CCCCCTGACG CTAGGCCATG ACACAACTAA ACTTCAATAC ACCAGGACTA 100
40 AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA 150

496

CCAGGCAAAA CCAGAACCTG A

171

(2) INFORMATION FOR SEQ ID :980:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15 TGATTCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC 50
CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC 100
CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG 150
20 ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATT A 200
CTGCAGTGGA AAATAACTGC ACTCTCAGGA CACAGCACTG T 241

25 (2) INFORMATION FOR SEQ ID :981:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :981:

TCACTGCAAT CACGGTAGCT TCGCCCAT TG CCTCTTCAAC CAGGCACATA 50
CATCGAGAAG TTGAACCTGC ACTTTATTTC AACTGAACA GACTTACCCC 100
40 GACAACAACA CCTCCCCAGT GGGACAAACC TACCCACCT CCCCACACTC 150

497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AACATTTGC 200

AAAACCACAC TTCAACCCAC AGGAAGA 227

5 (2) INFORMATION FOR SEQ ID :982:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG 50

ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT 100

20 CCGCGAACTC ATGACTGACC CCTTCTAAGT AAGAATCCCA CCCAGGCAAA 150

CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC 200

25 AAAAG 205

(2) INFORMATION FOR SEQ ID :983:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTTA AAAATGATCT 50

40 TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT 100

498

CCCAAATGAC ATTAAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA 150

CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC 200

5 CCCT 204

(2) INFORMATION FOR SEQ ID :984:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :984:

20 ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTG CATTCTTGTT 50

TTAAGTGATC TTAAATTGTA TATATCGCGG TAGTATGTTT AAAATCCACT 100

AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTGCT TTTTTTTTC 150

25 TTTCTCCCCC CTCCCCAG 168

(2) INFORMATION FOR SEQ ID :985:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID :985:

40 CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAA AGAAGCATGG 50

GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT 100

499

TTTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG 150
CTGGGAGGGG GGCCCTCACC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT 200
5 GGTCCAGCCC CTTACGCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT 250
CCTGATGTAT TTTTTTTTCC TCCAACTCAA AAGGCAAAAA TAATCCTATT 300
TTTATTATCT TGCTACAACT GCAACTTTCT GCCCTATAAA TTTACATTCC 350

10

(2) INFORMATION FOR SEQ ID :986:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :986:

AGCGACCGCC ACTCACTGTG AGTTCCAATT AATTCAGGTG AGCCGCTCTT 50
25 CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTTGAAGGT 100
TCAACAATGC TCTGCAAATC TTTTAAAGAC CCGTTACTTC AACAACTCCC 150
AATACCTTCC TCCTCAACGG AACRACTTAA CCGTTACCTT TTAAACCCGA 200
30 CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA 250
AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAA 289

35

(2) INFORMATION FOR SEQ ID :987:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

500

(xi) SEQUENCE DESCRIPTION: SEQ ID :987:

5 CACAATCATA GCATTTATTA CACGATTTAC ATCTGATCCT CACGCAATTT 50
TCTTCCTCAC CAATAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA 100
CATTCTTTTA TTCTTGCATC GCTATAAAGA ACTA 134

10 (2) INFORMATION FOR SEQ ID :988:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTTAGCTAT TGACTGTAGG ATTTGTAATT 50
CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA 100
25 ATTCCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG 150
GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT 200
30 TCATAATTTA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG 250
ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC 287

(2) INFORMATION FOR SEQ ID :989:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT 50
5 TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG 100
AATGACTCTC ACTGGCACTT TTAAACACAG CAAGCCCAAC ATATTTTCTC 150
CTTTTCATAA AGAAGCCTAT ACACCAT 177

10

(2) INFORMATION FOR SEQ ID :990:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :990:

TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA 50
25 TAAACTAACC CCACACCCTC ACCAACCAAA GGAGGCACAA TCCAACGAAA 100
CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAAC 150
CAAAAGTC 158

30

(2) INFORMATION FOR SEQ ID :991:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

TAATCCCTTT TAAGCAGAGA TACAC TTCA CAGAGAGAGA ATGTTTTAAA 50
AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTTAAT TCATTTTGAT 100
5 TACACAAAAA TAAGGCAAAC TAAATGATTG AGAACAATTC AATTTAACTG 150
AAGCCTTCTA GAAAAATACT CAACAGGCTT CAACAAAAG ACTTAGCGCA 200
CATAAAACAA TCACGAAGAT CACAATTTC GCACAAATAT CTGAAGGAAT 250
10 ACACGCAAAA CATCATA 267

(2) INFORMATION FOR SEQ ID :992:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :992:

25 AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACAGTGA 50
TTGTCAAATT CCACTTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT 100
CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA 150
30 TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA 199

(2) INFORMATION FOR SEQ ID :993:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

503

(xi) SEQUENCE DESCRIPTION: SEQ ID :993:

TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG 50
5 ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCGAGG 100
AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT 150
AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTACTGAAG ATGCGTCC 198

10

(2) INFORMATION FOR SEQ ID :994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :994:

GCTATCTGCG GGGCCATTCG TAGGATGGGT GAGTCAGATG ATTCCATTCT 50
25 CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGACTGGAGA 100
GAATAACAGA CGTGGAAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA 150
AAAAAAAAA ACAACAAACC CCAACAAACT CAA 183

30

(2) INFORMATION FOR SEQ ID :995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :995:

504

ACCTCTGCAT TAACACTCCA GCACCTTTGG TTAGCCAATT TGGCCTTATT 50
TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTTCG 100
5 GGTACCCCCA CTGTCCCCAA CTTCGAATAT GCTCACTGCC TGGAAAATGT 150
TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA 199

(2) INFORMATION FOR SEQ ID :996:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20

GGTCTTGGCT GGTGGTTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG 50
GTCCAATTTT CCACCTGGGG TTAAAAAGTT AAGGAGGACC AGCCTGGGAA 100
25 CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTTA 150
AGGGGACACC ATATGGAGAT TTTATGC 177

(2) INFORMATION FOR SEQ ID :997:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :997:

40

GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCATT 50

505

GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTTC 100
AGTGAATAAT TCCTCTTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC 150
5 GTAGAAAGTT GCTTGAAATT CTTTCTCTAA AAAAATTAA TTTTCTATC 200
TCAAAATGAC CGTATGCAAA CGAACATTA 229

(2) INFORMATION FOR SEQ ID :998:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :998:

20

TTGCAGTGTT TATGCCCGCC TTCTTTCACG GGCAGGTTCA ATTTCACTGG 50
TTTAAAAGTA AGAGACAGGC TGAACCTTC GTGGAGCCAT TTCATTACAG 100
25 GTCCCTTAAT TTAAGGAACA AGTTGATTTA TGCTACCTTT TTGCACGGTT 150
TAGGGTACCG CGGCCGTAA ACATGTGTTC ACTGGGCCAG GCGGTGCCTC 200
TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT 233

30

(2) INFORMATION FOR SEQ ID :999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

TCAAAACTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTGGCTT 50
CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA 100
5 TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAAA TAAACCACC 150
AGTGGAAGA GTTGTTGTG AGTTACATTC AAATACAACA GGAGTAATAC 200
TATCATGATA TTAGTT 216

10

(2) INFORMATION FOR SEQ ID :1000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

GACAAGACCT AGAAGCAACA ATGCCCAGTA GAAACAAACA CACCTACTGC 50
25 CTGGATCTTA GTTTTAATT ATATTCCCA ATAAGAGAC CCAGGGCTCC 100
TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA 150
CCTAGAATAT CTAATACTGC CAAAATTAA GAAAGTGTTT TAAAAAAAT 200
30 CCCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC 250
CCAATGGCCA AAGATCAAAT AATTTTCAA 280

35

(2) INFORMATION FOR SEQ ID :1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

507

(xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

5	TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC	50
	CTTATTTGGG GACTGGTCAC CAAAAATACC TAACTATGGT TGGAAGCTTA	100
	GTGCTTTTCAG CCCCATTTCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCCC AACTCCACAA GGACCCTTCC AGACCTCACC TGTGTATCTC	300
15	TTCATCTGGC TGTTCAATTG TATC	324

(2) INFORMATION FOR SEQ ID :1002:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

30	ATTTCATTTC ATAAGTCCTC ACAAACCCAC TTTTCCTCTT GCCTGAGTGC	50
	CTCACATACC CTA CTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCCC CCAGTCTTGC CTGCACTCTC	150
35	CTTTCCTCCC GCAGAGAGGC ATTCCTTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCCTCC TCCAGCAAGC TTCTTAATTC	250
40	ATTT	254

(2) INFORMATION FOR SEQ ID :1003:

508

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10

AAGGTTGCGC TGCCCATCCT CTCGCCCTTC GGAATTTACC CCTGGCCGCT 50

CAGGGTCTCG CTTCTAGAAG AAGATGATGG ATACTAGGGC GATCCTCCTA 100

15

TTGCCTTTAT ATTTAACAGG CCCGCCGAGG AGGGGCTCCC GCTGGTGCCC 150

ACATAACTCT ATTAGACCAT CTGAGGCGAC TTCCCCCACC CCCTCCAACG 200

CGCCTCACGC ACGACTCTAG CAAAAGACAG GTTCCGCGGT GGTCACGTCG 250

20

TTTGAGACTA TACTG 265

(2) INFORMATION FOR SEQ ID :1004:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35 AAATATGCCC TGAGGATTAT CTGATGTCGA TGGTGTGGAA AAGAACTCCA 50

GCAGGCGACT TCGATTCAA TCAATGTCCC CTGAATGCCA CAGAACCACT 100

AGCAGACGCT GCTCTCTCAG TCTTAATGGA GTGGCCTTCT GGGAACAGCC 150

40

GAGCTTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTTAA 200

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG 250

CCCCAGGTGA CCA 263

5 (2) INFORMATION FOR SEQ ID :1005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG 50

20 CTTCCATCTC ACTATTCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC 100

TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA 150

GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTTCGAATT 200

25 GTAAAATCGT GAGCCACTCA TATTCAAAC TAAAAAAGAA CAGAACTTTT 250

ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCAAA 300

30 CGCTTGCAAT CATAAAG 317

(2) INFORMATION FOR SEQ ID :1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTTCCTT GGAATGCCTT 50
TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCATCCTT AACAACTAG 100
5 CTGAGGTCTT ACCTCATCAG GATTGATCC CCCAAAAGA TTTGTCCCTC 150
TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA 200
TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA 250
10 GAGTCTTTGT CTAAATACTC AAAACCCTGT TTACCAT 287

(2) INFORMATION FOR SEQ ID :1007:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

25 GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA 50
CTGTCTCATC GGGGCACTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA 100
TGCTGTATTC AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG 150
30 TAAACTTTGA AGCCCTTTGA AGGACCTAAC CAAACAACAC AAGGATGAAA 200
ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA 250
35 TATTCGGATT TTACCGTAAG GAA 273

(2) INFORMATION FOR SEQ ID :1008:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT 50
TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC 100
10 CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT 150
GCGCCCTCTC CCTGCCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGGCA 200
15 TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG 250
GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG 300
CAAAAAAA 308

20

(2) INFORMATION FOR SEQ ID :1009:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
25 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

GAACCGCCTC TGTTTCCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA 50
35 GCAGTTTGA AAAGTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA 100
GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAATAA TGAGTGTAC 150
TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA 187

40

(2) INFORMATION FOR SEQ ID :1010:

512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10

AAGAAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG 50
ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA 100
AAAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT 150
AAGCTACTTC TCCTTGATAT TACCT 175

15

(2) INFORMATION FOR SEQ ID :1011:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

30

TGAAAAATAT TTGGAACCTCT TTAGTACAGA ACAGTTTCAA TATGAGTTAA 50
GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA 100
CAGAAGCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT 150
ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG 200
TATTTTAT 208

35

40

(2) INFORMATION FOR SEQ ID :1012:

513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10

ATGATATCTA GACTACCAGT ATTTTTTGAA TGAGGCTTTC TTAGGAGTAT 50
GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG 100
ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG 150
ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA 184

15

(2) INFORMATION FOR SEQ ID :1013:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30

CTTTGACATT TGATCAGACC AAACAGTGCT GTTCCCGGG GAGGAAACAC 50
ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC 100
ATACCTTGTT TATCAAATGA GCGACTCAAA ATGATTAAAA ATAATGCTGT 150
TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTATA TCTTTGTCAC 200
CGGAAAGAAG CATTTTGTAT ACTTTACTGC GAGTCAAAAA TCAATACGCA 250
GAATGGCATT TGA 263

40

514

(2) INFORMATION FOR SEQ ID :1014:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

CAAATTAAGT GCCAGAATGA TGCAGCCCGC TCTCACCAGG AAGAACCACA 50
15 TGTGAGAAAA CTTATAGCAG ATGCAAAAAT GTCAACCCAC CATGTTATTT 100
AAAAAAAAT ATGACCAGGA TACAAGGACA CTTACCGTT TTTAACCAC 150
ACAAGGTCAG GTAATGTTTA CCTTGAACA CAATCGCATA TGACCCTTTA 200
20 TGCCACTCAC CTAGGCCTTT AATAATGAG 229

(2) INFORMATION FOR SEQ ID :1015:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

35 GAAAATAATG ATTCATATTA CCGGGTATTT CTTATCCAGT CTTTCATTCT 50
ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG 100
TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC 150
40 ATGCACATAT ACACACACTC ATAGAGAACA AAATTATTCC GAATATTTCA 200

515

TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA

246

(2) INFORMATION FOR SEQ ID :1016:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15 TTCATAATCG CTGGCACTGA ACAAAGTTGC AGAATTCTTT GCCAGGTACT 50

TTAGGAAATC GTGAAGATAA TTGAGTAATA AAGCAAGGCT CTTCTCATCC 100

AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG 150

20 ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA 200

GAATTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC 250

25 AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA 287

(2) INFORMATION FOR SEQ ID :1017:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA 50

40 CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTTGAA ATGCTGTTTG 100

516

TCAACATTTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG 150
TTAACCACAA TCAGTTCTAC ATAATTAAAC AGAAAACATC TGGTGGCACT 200
5 TTTAAATGTT TAAGGACAGC ATTCACAAA CTAAGCCCGC CCCCAGTCCC 250
ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA 299

(2) INFORMATION FOR SEQ ID :1018:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

20

ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT 50
GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT 100
25 TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG 150
TGGGTTTGAG GTGGGCCCAA GAATTTCCCT TTTTAACAAG TTCCCAGAAG 200
ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTTC 250
30 AAGAGGACAA TCTAAAGTGC TCCC 274

(2) INFORMATION FOR SEQ ID :1019:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

	TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA	50
5	CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC	100
	GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG	150
	CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA	200
10	AAATGGCACC TCATCTTTGA TCAAAGATTC AG	232

(2) INFORMATION FOR SEQ ID :1020:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 133 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25	AACAGTCCAT GCTGATCTTA GTAACATGA TGAAGATGGT GCTTGGCCTG	50
	TTCTTCTTGA TGAATTGTT GACTGGCAAA AAGTCCGTCA GACATCATAG	100
	CAAGAACTAT GTGAAGAAAA TGCAAACCTT TAC	133

30

(2) INFORMATION FOR SEQ ID :1021:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 280 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT
ATTTAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG
5 ACTGTTGAAA GTTTAAGTAT TAGTAACTT GAGTTACTTT TTCTTTCAAA 150
TTTCACTCCG CTTCCCTGCA TTTCCAAGCT GCTCTTTCTG GTCCTACCCA 200
CCACCCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA TTTATCAAGG 250
10 TATTGGGGAT CCATTGTCTA TATTTAAAC 280

(2) INFORMATION FOR SEQ ID :1022:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

25 AAAATAAATA ACTTCTTAGA TTTTGGACTG AAAAGATCTG AGAATGTTCT 50
GCCAAACAGC CGACCAACTG GTGCAAAAGG TTAAGGCTGA CTTGACTTAG 100
CAACCTGCAG CACAACCAAA AACACTGATG CAGTTCAGAG CTCTTCAAAT 150
30 GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA 200
ATCCTCTAGA CAGTTTTCTT TTTGTTTGC ATGCATCCCG TTCCATTTTC 250
35 ATTACGGGCA TCTATTCCTT GATCAATTAT GTGCTTTGCT TTTTAATCGG 300
TTTT 304

(2) INFORMATION FOR SEQ ID :1023:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs

519

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

10 TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA 50
CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC 100
GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG 150
15 CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA 200
AAATGGCACC TCATCTCTGA TCAAAGATTC AGAGCAT 237

20

(2) INFORMATION FOR SEQ ID :1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

GGCATGATTA TTAGAACTA TTAAAGCTTT TTTCTTTGAA AAACAAGCTC 50
CTTTTACAGA ATATAAACAA CAGTAGTGCC TGTGGTTTAG CCCACCAATC 100
35 TTGATGACTA AAAGTAGCTG ATGCATTGTG CATATGATGC TTGAGATGGT 150
TTTTGCAAAA GCAGAAATCG CTGCAAGGTA ATCACAATAG ATAAAAGTGG 200
TATTTTAAAC CTTTGAAATA AATGGATGTA ACTGTACCTT GGTACAGCTT 250
40 TTCATTGTT TAGTTTTTAA ACGTTAGTAT AAGATTAGGT AATTGAGGGT 300

520

TAGAGCCAAC AGGAATCTGC

320

(2) INFORMATION FOR SEQ ID :1025:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15 TTCTGGCACC ACATTCAATA CTGATTCACA GGGATCTAAA ACATTCTAGT 50
TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA 100
ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG 150
20 TTCCACAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT 200
CT 202

25 (2) INFORMATION FOR SEQ ID :1026:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

ATTGGTAGAC AATATCATAA GAGTTTTCTG ATAAAAGATG CTTTTTAACC 50
CTGACTCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA 100
40 AACTTATACA TTTCATAAAC TAAAGGTCAT CCAAACACTG CCAAAAACGT 150

521

TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTTCC AAAGAGAATA 200

CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA 243

5 (2) INFORMATION FOR SEQ ID :1027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTTCCA ATGCACAGTT GCCACATTTA 50

GTCCTGACTG TAGGAAACAC TGATTTTGTA AAGTTGCCTT TATTTGCTGT 100

20 TAACTGTTAA CTATGACAGA TATATTTAAG CCTTATAAAC CAATCTTAAA 150

CATAATAAAT CACACATTCA GTTTTAAAAA AAAAA 185

25 (2) INFORMATION FOR SEQ ID :1028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC 50

TTAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG 100

40 AGCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG 150

522

TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG 200
TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCCT TCTCCTCAGC 250
5 CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT 300
CTGTTCACAG TT 312

(2) INFORMATION FOR SEQ ID :1029:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

20

ATTATTTATA AATTTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT 50
TTGAATTCAA ATTCATTCAA AAGTTGCACA AATTATTTC TTTTTCCTG 100
25 AACATTCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT 150
TAAGAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA ACTAGAATTT 200
TATACAGATG GAAAAAGA 218

30

(2) INFORMATION FOR SEQ ID :1030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1030:

523

TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTTAAAC ATTGAATAAA 50
ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT 100
5 TTCTTAGTTC TTTGGACACA TCCG 124

(2) INFORMATION FOR SEQ ID :1031:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTTCAGTC TGTAGCTTGC 50
20 CTTTTTATTT NTTAATGGGT ATCTTTAAAA AAATGGAAGT TTAAAGTTTG 100
AATGGAATTC AGTTTGTTTT TAAAGCTTGT GCTTTTGTG TTCAACTAAG 150
25 GGATATTAGC TTACCATTTT TCTCGGTGA ATATTATGTG TTTATAGACA 200
AGAAATGGTC ACTAAAGCAA ATAAGTAA AATTATC 237

(2) INFORMATION FOR SEQ ID :1032:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1032:

40 ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCCGAGT TCTAAGGCCA 50

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA 100

GCGACTTCCT TGAAGACTGT TTTTAACATA CCAAAGGAGG ACAAGCT 147

5 (2) INFORMATION FOR SEQ ID :1033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double.

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA 50

GAGGGGGGCA CTAGAAGCAA TATCTCCGAA ACTTCTTCGA CTGTCGAGAC 100

20 TTTTACTCA TAATTCGCTT CAAGCCAACT ACGGAGGCGC ATTTACAAAA 150

CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA 200

25 TCCTCTGTCC CTACTCCCTC TCCTAGGACA CCGCATTA 238

(2) INFORMATION FOR SEQ ID :1034:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT 50

40 GGACTGTGCA GGG 63

525

(2) INFORMATION FOR SEQ ID :1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCGC TCAATGGCGA AATCCGAGC CAGAGCTATT GGTGAATGA 50
GTAGCGCTGA TGGTTTAGAT AATAACTAGT ATGGGGATAA GGGTGAGCAG 100
GCGCGCCTTG AGGCAAGAAG CGGGTTAGAG CATCTCTACT TAAAAGCCA 150
AAGCCTATAA CGGTAGCGTC TACATCACGA 180

20

(2) INFORMATION FOR SEQ ID :1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA 50
CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA 100
CAACGGCGAC ACTCGACTAA CCATTTTAAA CCAATTGGAA CC 142

40

(2) INFORMATION FOR SEQ ID :1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs

526

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC 50
TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG 95

(2) INFORMATION FOR SEQ ID :1038:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 195 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

25 ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT 50
TTGACAAAAA CATAACACA TAGTACAGGT AGAACATATA ACTGGTTGAT 100
GCTAAATAAC AGATCCAGAT AATTTTCAAT TTGAATTAGC AGCAGGGAGT 150
30 CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT 195

(2) INFORMATION FOR SEQ ID :1039:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

527

(xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

	GGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGAAGACAT	50
5	TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTT TAAGATGAGG	100
	TTAAGTTTCT TAACAAAAGA ATAAACAACG GTGACTCTAT CTGTCGGGGG	150
	AGGGTCTAGA CAGAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA	200
10	CGAGACTTTG ATGGAGAC	218

(2) INFORMATION FOR SEQ ID :1040:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 318 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1040:

25	TTTATTATTT TGAATGATTT AATGGTTTTT TACACAATTT ACATCACAAC	50
	ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATTC	100
	CTTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG	150
30	CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTAAAGATG	200
	CAAATGCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA	250
35	CAAGTCCTAC AATTTTAAAA AGGCTCGATG GAAAAATTC TCAATCCTGA	300
	AATCCCCTAG GGAAGGGG	318

(2) INFORMATION FOR SEQ ID :1041:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 199 base pairs

528

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

ACGTACCGAG CCGTCGTCGC GGTGCTTGAG CTTGAAGGCG AGATAGCCGA	50
10 TGCCGCCGAG GCGGTGGACC GCATCACGGT GCGCTGACG AACGCGAGAT	100
TCAGCAGCAG CGATGCCATC AATAGCAGCC TGATCGGACG CATGACCGAC	150
15 TCTCCCTGTG AGCGGAGGTT GGGGGGCCGA TCTCCGCCG GTGCCGGGC	199

(2) INFORMATION FOR SEQ ID :1042:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 300 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

GCCTCTAACA AAAGTAGGCT GTCCCGGACC ATGGTAATAG AATTGTTTAC	50
30 CTTTATACCA AGAAGGTTGG GAAAGCACCA AAATCTGCAT GTGGTGTGTG	100
CCCAGGCAGA CTTGAGGGG TTCGTGCTGT AAGACCTAAA GTTCTTATAG	150
35 ATTGTCCAAA ACAAAGAAAC ATGTCAGCAG GGCCTATGGT GGTTCATGT	200
GTGCTAAATG GTTCGTGAC AGGATCAAGC GTGCTTTCCT TATCGAGGAG	250
40 CAGAAAATTC GTTGTGAAAG TGTGAAGGC ACAAGGCACA ATGTCTGGAA	300

(2) INFORMATION FOR SEQ ID :1043:

529

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

10

GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAGAGA 50
GTCTGGGATG AAGCGGCCTC CTCCTGTCT TGCCCTCCAA AATTGAGTCT 100
GGCCTGATTC CTTTGAGGAG CAAATTTTAC AATCATCCCT CACCCTAACA 150
CACGGTGAAA CTGGAACC 170

(2) INFORMATION FOR SEQ ID :1044:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

30

GGCCCCCCT GGGGACTGCT GGTTCAGG GGCCACCCC CCTCATCCAA 50
AAGAAGAATC AAGTTTTGTT TTCCTGTGGT TCCCTTGCTC TCCCCGGCCT 100
CACCTCGAGC TTCCACTTGG GCCCTTCCC ATGCTTCTAC TTGAGCCCCG 150
CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT 200
GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCTAT 250
TTTTTTTTTT 260

40

530

(2) INFORMATION FOR SEQ ID :1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA TTTTAAGGGC TTAACCTGTG ACTTTAATAA GCTGGAACAG 50
TCCACTGAAT GGGTATAATG AATTGCAGTA TATACGTATG ATCGCTTTTT 100
AAGTGATTAT CTTTTCTTTC GTTAAGTCAT GTAAATTCAT AAATTTTTTG 150
GCACTGATGT GTTG 164

20

(2) INFORMATION FOR SEQ ID :1046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

TCCCTCCTTT CCGAACTGGA GCCCATCCT CTCCAGAGTA TCCAGGGCTT 50
CTTCACTCCC GGGTACCTGC CCTTCGGCCC CTTTTCACCA CAGCTGTGCT 100
ACTGTCAACC AGTCTTTGCT GCATAGGCAT 130

35

(2) INFORMATION FOR SEQ ID :1047:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

531

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

10	GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC	50
	AGTGGAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTTGA	100
	CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG	150
15	TGAATCTCCA TTCGAGGAAG GGGAAGAAGA GCTCGGAGGG TGACAGCCTC	200
	CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCTT CTCCTCCTG	250
20	ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA	285

(2) INFORMATION FOR SEQ ID :1048:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 233 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

	TAAAACTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA	50
35	CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC	100
	CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC	150
	GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC	200
40	CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA	233

532

(2) INFORMATION FOR SEQ ID :1049:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

ACTTTAATTT ATTTCCGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC 50
15 TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG 100
AACTCTGAGC TGTCTTTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC 150
TTAATTCCTC ACGACTCAGA AATGTTAACG GCACTGTCTGA GTGCTGTGAT 200
20 CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTT 250
GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTCGGTCTGA TAC 293

25 (2) INFORMATION FOR SEQ ID :1050:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

AAACTATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA 50
GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTTGGCA GATAAATACC 100
40 AGATCAAAAG TCCTGTTTCA GTAATTTGAT TAACTGTAG AATACTAAAA 150

533

AATAAGTTAT TTCTACAGAA ATCTTTGAAG GGAGCAAAAA ATCAAATCAC 200

AGTATATACC TAATGGCTA 219

5 (2) INFORMATION FOR SEQ ID :1051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATTCCGTGC AGTGTTTGAT TTTTCGTTT 50

TGCGATAGTT TACTGAGAAC 70

20

(2) INFORMATION FOR SEQ ID :1052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC 50

35 CTGCCGATGA TTTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC 100

CTTCCAGAGA AGATAGGATG TGAGTGAGTA AGTTATGTAT AATAATTTTA 150

TCTCAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG 200

40

TATT 204

534

(2) INFORMATION FOR SEQ ID :1053:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

ACTAAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT 50
15 AAGAGAGGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG 100
AGGTATAAAA GGTATCCAAG AAAAGTAAAA CATACAAAGG CAATTCAAAT 150
CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC 200
20 CATACCCGAC AGAAAGTACC GGAATACCAC CGACACTGAT GTCTTCCAAA 250
CG 252

25

(2) INFORMATION FOR SEQ ID :1054:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA 50
CATCTGCTTA TTAAACACTG AAGTAAAGA ACTAATCCAG TTTGCAGTCT 100
40 TTAGAGGTGT TTAGTATTTT ACTCCGTTCT GATGGAAGCA CTTTGAATGC 150

535

TTGCATGGAG ACATAAACT GAATATTTAA TTGACAATAG ATCATGCGCC 200

TGTATTATA AA 212

5 (2) INFORMATION FOR SEQ ID :1055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

ATAAACTGTG CTAATAAG TTTTATTTT ATCAATATAA AAGCTGTAAA 50

AAAACTGAGG AGAAAGCAGT TGCCAAAAAG ATGAAAGAAA AACAACATAG 100

20 AAAACCTTTA AAACAGGCAA AAGTCAGTTC ATAATAAGT AACTCATCTC 150

AC 152

25 (2) INFORMATION FOR SEQ ID :1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGT 50

GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG 100

40 AGATGTTGTA GTCGGAGCCT CATTCCTTCC GGGGCACTGT TTCTTCTAAT 150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG 200

GCAAA 205

5 (2) INFORMATION FOR SEQ ID :1057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC 50

CCTTTGTCTG TTAAATACA CTGGGAGCCA GAGCTGATTC CCCACCTGCT 100

20 GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT 150

GATAGCAGGT TTAAAATGA ATCC 174

25 (2) INFORMATION FOR SEQ ID :1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA 50

GCTTTAAAAT ACCATGTTGA CAGCATTTTG AATTGTTTCA TAGACGTACT 100

40 TATTAACTG ATGCGAACAT TCACA 125

537

(2) INFORMATION FOR SEQ ID :1059:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTTCA AATACTGTCT 50
15 TAGTATATTA AACTCTTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC 100
GTTGAAACT TAGGTTTGTT CCTTCTAAAA TTTCTAAGTC CTCATTATG 150
ACTATAAAGA AAAAAGGTTC ATCAATTCAA AAAAAATCC TGATTCTTCA 200
20 AAATA 205

(2) INFORMATION FOR SEQ ID :1060:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

35 ATCTCACAGA TTCTTTTCA CAGATTCATT CATGTTGAGT GAAAGAAGCC 50
AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTTG 100
AAAATAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG 150
40 GTGAGTGTC TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT 200

538

ACTTGGATT TGGGTCTA: 3CTGGCAGG GGAAGGGTA CATTGCAAA 249

(2) INFORMATION FOR SEQ ID :1061:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

15 TAGCACATTG CATCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA 50

AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT 100

GCAGAATCAG TGCTTGAAAA AGGAGAAAGA GAGATTTTCT TTACAAAAGC 150

20 TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC 200

(2) INFORMATION FOR SEQ ID :1062:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

35 GCGCACAGCT GAGAATCTCC GGTCTTGTCT CACTTTGGAC TGGGACAGTG 50

GATGCCCATC TAAAAGTTAA GTGTCATTTC TTTTAGATG TTTTACCTTT 100

ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG 150

40 ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTTCCT 200

539

(2) INFORMATION FOR SEQ ID :1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

TATCAAATCA TGAGTTGAAA GATTTTGACT ATTGAAAACC AAATTCTAGA 50
ACTTACTATC AGTATTCTTA TTTCAAAGG AAATAATTTT CTAAATATTT 100
GATTTTCAGA ATCAGTTTTT TAATAGTAAA GTTAACATAC CATATAGATT 150
TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC 200
AAATTCAAAT CTCAAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA 246

20

(2) INFORMATION FOR SEQ ID :1064:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

CCCTCATGTG CCAGTTCGGT CTGCCTGCAG AGGCTGTGGA GGCCGCCAAC 50
AAGGGCGAGT GGGAAGCGTT TGCAAAGCCA TGCAGAACAA CGCGCAAGTT 100
TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA 150
TGGAGCCTGG ACTGAGCCAC 170

40

540

(2) INFORMATION FOR SEQ ID :1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTTCATT 50
GACCTCTGTG TGTCTTCAGT CCTTGACCCT TTAAGGCTCC CTGGTGCCAG 100
AATGTCTGCA GCTGTAGGAT CAAAGACCCT TGGGGGAAAA ATCCATTCTC 150
AAAAGAGAGG AAGATGGGGT G 171

20

(2) INFORMATION FOR SEQ ID :1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT 50
ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAGC 100
TCATACACAG CTTTCATGGGT TTA CTTTCCC AAGCACTTCC TCCCTCCCTG 150
CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTTCC CCTTTTCAA 200
C 201

40

541

(2) INFORMATION FOR SEQ ID :1067:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT 50
15 GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG 100
GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG 150
C 151
20

(2) INFORMATION FOR SEQ ID :1068:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTTG 50
35 ATCTGTTTGC TCCTTTGAGT CTCCCTTTTA CTTTACAACCT AGAAAACCAA 100
TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC 150
TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTTA 200
40 AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTTGGAA 250

542

ACTGACTTTA AAGAAAACAT ACA

273

(2) INFORMATION FOR SEQ ID :1069:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15 CAATCTTGCT TATAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCAT 50
TCCTGGTGCA ATTGTGATTT TTTTGTAGCC AAAATGAATG GCAAACCTCTA 100
TTTAGAGCAA AGTAAGTATT AGAAAACCTT AGGAACTCTT AATCAACGTT 150
20 TATTACACTT TTATAAAGGC AACTACGCG AAAGAGCCC 189

(2) INFORMATION FOR SEQ ID :1070:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35 TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT 50
TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG 100
TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC 150
40 ATGAATCAGC ACTTCTCATC CCGTTTTATC AGAGTGCATA TACGTCCTAC 200

543

TTAAGGAAAA GTAAACAGT CATTTACGAA AGAAAGTCAA TCTGTATCCT 250

AAGCATTTTA ATAAAAAGTC AGAAGGAATT 280

5 (2) INFORMATION FOR SEQ ID :1071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC 50

TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTTGAAA 100

20 GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA 150

GATGCGCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG 193

25 (2) INFORMATION FOR SEQ ID :1072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCAGATA GGCCACGCGC 50

AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC 100

40 CACTCTGCAG CCATAGGCCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG 150

544

TCAAGTTCCC CTCGAGATTC ACATC

175

(2) INFORMATION FOR SEQ ID :1073:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15 AGTGGCCCTAC TCTTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG 50
GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG 100
GTGGACAGGC TAATTTTCC TTGAAATGT GGCTTCTTCA ACTCCTTTCA 150
20 AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT 200
TCTCTTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA 250
25 TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA 300
TCTATATAGC ACATAGTGTT TAAAGACTAA TGAATGCAA 339

(2) INFORMATION FOR SEQ ID :1074:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1074:

40

ATTAATTATG CGGTCCTCCT CCTGGCAGCT GGACACCAGT TTGAATCTTC 50

545

CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA 100

ATCAAGAAAC TCGGACCCAA CTTGGTGCAA AGACGGATCT CCGCCGATTC 150

5 TGACGGCTCT CCAGGTTTTG TC 172

(2) INFORMATION FOR SEQ ID :1075:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

AGAGTAGGAA GAGGGAGGGG AACAGGCATC TAAGATAGAC TTTCTCCATC 50

20 TGTGTTGGGAGC CTGGGCAAGT AGGAAAGAAG CCTTTTTCAT ACACTTCAGT 100

CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGGCAG 150

25 CCTGCAAATG AGACCACTCT CATTTCTCAG TTTCGATTTG ATTCACTCAC 200

TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG 250

GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACGTTG CTA CTGATG 299

30

(2) INFORMATION FOR SEQ ID :1076:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

546

	GGCCTCATCG GCGATACTGG AGGTTGCTT TCTCAACCCT GTGGGCTTCA	50
	CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC	100
5	ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG	150
	AATGCCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG	200
	CGAGGTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA	250
10	TCATTGGAAG TATTGCTATG AGCACTGCGA AAA	283

(2) INFORMATION FOR SEQ ID :1077:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 297 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

25	ACCAATCAAG TAACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC	50
	AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAACTC GAATAAGAAG	100
	TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA	150
30	GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA	200
	GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTCAGGC TGGAAACTA	250
35	TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC	297

(2) INFORMATION FOR SEQ ID :1078:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 291 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

AATCTTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC	50
AGTGATTGAA CCTTTATTAT TTACCAGCTA ATATAGTAGG CCCATAAATA	100
GGTTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG	150
TAGCGCTACT ACCCATACCT GCTAGCAGTC AAGGTTGAGA TAATCATAAC	200
ACGCCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA	250
GTTTATATCT AAAGCCCATG TTCTTTTGCT TAATATTAGA G	291

(2) INFORMATION FOR SEQ ID :1079:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1079:

30

AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAC ATAAGCGGGG	50
CTCACTCACC CACCACATTA ACACCACGAA ACGGGTAATC TAACACGAGA	100
AAACACCCTA ACGTTCATAC ACCCCATACA CCATTA	136

35

(2) INFORMATION FOR SEQ ID :1080:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT 50
GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA 100
10 GCTGCGGTAT TAAAAAATC AAGAATGGAA GCGTTCCTCA ATTGTCGTTG 150
AGAATCATAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT 200
15 CGCGCGTTTT TCATGGTTCG CATCTGCCGT GTATGCAATG ATTCTCAACA 250
CACATTGGAG TCACGCGGCC TCGTAAGAG TATGAAGGTC TTCCTGTAAA 300

(2) INFORMATION FOR SEQ ID :1081:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

30

GTTAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAAA GTTTTACTAA 50
AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT 100
35 ATTGGATGAG ATTTGTTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC 150
TGAAAATCTC TAGACATTG CTGAAATTGA TGAGAGCATG CACAGGACGA 200
CTGAAGGTGC TGGACATGA 219

40

(2) INFORMATION FOR SEQ ID :1082:

549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

10

ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG	50
AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG	100
CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT	150
GCAGCACAGG CGTGTATCCT CTCCAAAAAG CTGCTGCTCA TTTCTGGCCC	200
CATCTGCTGC TATCTTTGCC AGTCAGCCAT CACAGTTTGG CATCATCAGA	250
GTCTCAGCTA GAGGGAGCGT GTCATTCTG CCTTAGTGGT TTGCCTGCCA	300
CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACTT	350
GTCGGAAGTT	360

25

(2) INFORMATION FOR SEQ ID :1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT	50
CTTCAATTA AATACTACTCC AAGACATCGA GTTTGGCAGA TATTGCGCCC	100

40

550

GCCGTTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT 150
AGACATTTGC TTGAAATTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT 200
5 GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAAAAA AAAGTTCAG 250

(2) INFORMATION FOR SEQ ID :1084:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

TNCTAGATAC NTCCCTCTGT CTCACATTCA TAGTGTGTTT TGTCTAGTG 50
20 TATGAAGTCT CACNCAAGGA AAGTGTNCAG GCAGAGTTTG GGGAGAGTGA 100
AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG 150
25 GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTTAAA 200
AAATTAAAAA GAGGATTTTT AAAAGGAATA TCTTGTTCAA AATTNTTAA 250
GTTTAAATAG G 261

30

(2) INFORMATION FOR SEQ ID :1085:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

	GCAATCCATA AGTGTCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT	50
	CTTCATGATC TTTTTCGATT TTAAATGTC ATGCAATTTT AGAGAAAAGC	100
5	TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA	150
	TCACTTTTTC ACTTCCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC	200
	TTAATACACC AGACAAGAAC AACTATGAA TGCAGACAG AGGGAGACAG	250
10	AGGCGAAATA	260

(2) INFORMATION FOR SEQ ID :1086:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 213 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

25	AAGACGTGGA TTGCTGGAA GACACGGATT TCCTGGAAGA CCTGGATTTT	50
	TCGGAAGCTA TGGATTTGAG GGAAGACAAG GATTTTCTGG AAGACATGGA	100
	TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA	150
30	CGAATTCCT GGAAGACCCG GATTTTTCGG AAGCTATAGA TTTAAGGGAA	200
	GACAAGACGG ACT	213

35 (2) INFORMATION FOR SEQ ID :1087:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 256 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

552

(xi) SEQUENCE DESCRIPTION: SEQ ID :1087:

5 TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG 50
TTTAGGCATT TGGAAAATCT GGTTCACATC ATAAAGAACT TGATTGAAA 100
TGTTTTCTAT AGAAACAAGT GCTAAGTGTA CCATATTATA CTCGACGTCG 150
10 ATCATTCTC AGTCCTATTT CTCAGTTCTA TTATTGAGA ACCTAGTCAG 200
TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT 250
TTTTTT 256

15

(2) INFORMATION FOR SEQ ID :1088:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1088:

TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC 50
30 TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCCAGACAG GGAGACCAGG 100
GCTCTGACAG TGACAGGTTC TTCCCTCTGA AAAAAGAATA GAAGAGGAGC 150
TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA 200
35 AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA 250
CTGAGGCGAG AGGC 264

40

(2) INFORMATION FOR SEQ ID :1089:

(i) SEQUENCE CHARACTERISTICS:

553

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1089:

10	GACCTGGAAT TTGTTTTCGT CTGTTACAGTA GACTCCGATT TCAGAATATG	50
	TCGGAATTTC AGACTCCGGA ACTTTTGAGA ATGTCATTAC AGGAACTTTG	100
	TTTACATACC GAGCTGTTAG CCCAGTCAC TGGGTCCGAA ATTACGCCGA	150
15	TACCGAC	157

(2) INFORMATION FOR SEQ ID :1090:

- | | |
|----|-------------------------------|
| 20 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 366 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1090:

30	GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA	50
	CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT	100
	AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAACT CGATGAGAGA	150
35	GAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTTGGT	200
	CAAGTAATGG AAACTTTTGA CTACTAGTGT AAGTCAAAAG ACAAAGGACT	250
40	CCAGCAAGAT GAGAGATTTT TCTATTTTGT AACGAGTAGT CCACCGATCG	300
	TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAAAA	350

554

AAAAAACATA GATGTT

366

(2) INFORMATION FOR SEQ ID :1091:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15 GGTCTGAATC ATGAAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC 50
AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTT GCTCTTGTC A 100
CACCATATGA AGACATCAAA AAACACTTAA GGATTCGAGA AAGAGAACAT 150
20 CTTTTGTAA AGAAGAGAAT AACATTTTGG AAGAAAAAGT AATAGCAAAT 200
TTGAAGAAGA AACAAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA 250
25 TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTG AAGAGCAAAT 300
GGACA 305

(2) INFORMATION FOR SEQ ID :1092:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1092:

40

AAATGGAAGT TGAAGTGAAGT GTGGTTTCCA GTACAGGGCA TCTGGCCACC 50

555

TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT 100
GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTTG 150
5 CTTCTTTATT TTTATTATTA TTATTTTCT TTTTGTGGAG AACAGCGTCT 200
TGCTGTATTG CCCAGCCTGA TCTCAAATC CTGGGCG 237

(2) INFORMATION FOR SEQ ID :1093:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

20

AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGAAGTGCA ATATCAAGGT 50
GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA 100
25 GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA 150
CAGTCTTCTC CATGTGTATC CTTCTTCAG TTTCCCTTAT AGGACACCAG 200
TGATGTCAGA TTAGGGATCG AACCAACAA CCTCATTTGA AGTTACTCAC 250
30 CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTA GGAAGTAGGA 300
CTTAGGGCTT ACAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTTA 350
35 AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATAACACA TTAAGGTTTG 400
TGGGATTCAG AAAGGTATAC 420

(2) INFORMATION FOR SEQ ID :1094:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

556

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

10	GTTCCTTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA	50
	CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTT TCCATAGGAG	100
	GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC	150
15	AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT	192

(2) INFORMATION FOR SEQ ID :1095:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

30	AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT	50
	ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCTCCC	100
	ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTTT CACCAGCATT	150
35	GCCAAACCAC TTGGGATTCC TGCGCATGGC TTTGCTTAGT TTGCTCTTCT	200
	GCTTCTTGGA TACCTCCTTC AGGAAATC	228

(2) INFORMATION FOR SEQ ID :1096:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs

557

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1096:

ATTTTTTATG GAAAAAGGGG GATAATGCAA AATAGCAAAA ATTGTAAACA 50
10 AAGTTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TAAAAACACC 100
TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTCATTAC 150
15 ACTGCTCCCT ACGCATGAGA AAGACCAGAT GTCTGGTTTC AGAGTATT 198

(2) INFORMATION FOR SEQ ID :1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1097:

TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG 50
30 CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTCTAC AAAACTGTGA 100
CACTTCAGTC AGTTTTTC 118

(2) INFORMATION FOR SEQ ID :1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

558

(xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

5 AAAACTGACT AAAGTCANTG TGTAATACGA AAACCGAACA CTCCAGCAGT 50
CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNGGGACTCG 100
TCNCAGGTGT TTNGNACTTG CCGCCCGACN GGCNAAGG 138

10 (2) INFORMATION FOR SEQ ID :1099:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

ACTCCACCAC TGGGNCCGCC ATGTTTGGG TNGGNGCAAT GCGCTGTCTG 50
TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT ACACTGACTG 100
25 ACACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG 150
G 151

30 (2) INFORMATION FOR SEQ ID :1100:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT 50

559

CGTGTAAGTA CACTCTATAT TGGCACAACA TAAAATTAAC TAGTGACGCA 100
TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT 150
5 CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG 200
C 201

(2) INFORMATION FOR SEQ ID :1101:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

20

TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT 50
CGTGTAAGTA CACTCTATAT TAGCACAACG ATAAAATTAA CTAGTGATGC 100
25 ATTTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG 150
TATCACTGGA GGACTGGGNC CAGGACCTGA CCTGGTGGTA CCAAAATCCA 200
TGAGGCNGNA AT 212

30

(2) INFORMATION FOR SEQ ID :1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG 50
GTTCTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT 100
5 GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC 150
AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN 200
GAGTGGAAT TCCANCAT 218

10

(2) INFORMATION FOR SEQ ID :1103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT 50
25 TCGTGTAAGT AACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG 100
CATTTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA 150
GTATCACTGG AGGACTGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC 200
30 ATGAGCG 207

(2) INFORMATION FOR SEQ ID :1104:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

561

(xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG 50
5 ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC 100
TCTGCCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCTGAAC 150
AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT 200
10 CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN 250
GTGNAGGCC 259

(2) INFORMATION FOR SEQ ID :1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

ACATGACCCC TTGGACTGAA GCGCTCAGT AGTAAAGGAG TGTCATGCAG 50
GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA 100
30 CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG 150
CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC 200
35 ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT 230

(2) INFORMATION FOR SEQ ID :1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

562

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

ACATGNCCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT 50
CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA 100
GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG 150
GTNAGAGGGG GCT 163

15 (2) INFORMATION FOR SEQ ID :1107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA 50
GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT 100
GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA 150
GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT 182

35 (2) INFORMATION FOR SEQ ID :1108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

563

(xi) SEQUENCE DESCRIPTION: SEQ ID :1108:

5 CCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTCATGC AGGTCAACAC 50
ATGTCGCACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT 100
TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG 150
10 AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTTGTTT 200
CGNGCCTTGA AAGA 214

(2) INFORMATION FOR SEQ ID :1109:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

25

ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTTCATGCAG 50
GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC 100
30 ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT 133

(2) INFORMATION FOR SEQ ID :1110:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTGATG 50
CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA 100
5 TGCACGGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT 150
GGAATG 156

(2) INFORMATION FOR SEQ ID :1111:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1111:

20

GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCCG 50
AGGTGCCTCA AAGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC 100
25 ATNAAGGATG TTATAGATAT ATCCAAAAGA AATAAATCA TTCTTCAAAA 150
AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT 200
CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT 250
30 GCATACACCA CGAAATACTA CGAGCCATAA AA 282

(2) INFORMATION FOR SEQ ID :1112:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

565

(xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

TAATTAGTTT AACCAGTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA 50
5 ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT 100
CAAAAGGAAA TAAANNGNCN TGTNAAAGAC CATAACNAT NGTCCATCGG 150
AGCCCGTATN CACGCAGCTT GTCATAACTA T 181

10

(2) INFORMATION FOR SEQ ID :1113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG 50
25 AACTTAAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA 100
TAGATATATC CAAAAGAAAA TAAATCATTC TTCAAAAAGA CACATACACT 150
AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA 200
30 CACTCATGAA TCGGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA 250
AATACTACGA GCCATAAAG GCGAAATC 278

35

(2) INFORMATION FOR SEQ ID :1114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

566

(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

ACCTGCAAAC TTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50
5 TGAGCCATAC AGTTTTTGT GCAACTAGTC AACTCTCAAC TNACGTGGAC 100
AGCATGTAAA GAACGAGAGT GACTG 125

10 (2) INFORMATION FOR SEQ ID :1115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCGGGA CCTGCAAAC TTTTGAAAG 50
ACCAGATAGT AAGTATTTTA TGCTTTGTGA GCCATACAGT TTTGTGCAA 100
25 CTAGTCAACT CTCAACTCAC CGTGGACAGC ATGTAAATGG ATGGGAGTGG 150
CTGCCGG 157

30 (2) INFORMATION FOR SEQ ID :1116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAAC TTTTCTGTAA AGACCAGATA GTAAGTATTT TATGCTTTGT 50

567

GAGCCATACA GTTTTTGTG CAACTAGTCA ACTCTCAACT NACGTGGACA 100

GCATGTAAAG AACGAGAGTG ACT 123

5 (2) INFORMATION FOR SEQ ID :1117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTTTGTG AAGACCAGAT AGTAAGTATT TTATGCTTTG 50

TGAGCCATAC AGTTTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC 100

20 AGCATGTAAA TGGATGGGAG TGGCT 125

(2) INFORMATION FOR SEQ ID :1118:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

35 ACCTGCAAAC TTTTCTGTG AAGGACCAGA TAGTAAGTAT TTTATGCTTT 50

GTGAGCCATA CAGTTTTCGT TGCAACTAGT CAACTCTCAA CTCACCGTG 100

GACAGCATGT AAATGGATGG GAGTG 125

40

(2) INFORMATION FOR SEQ ID :1119:

568

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1119:

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT 50
 CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT 100
 CAAAGAGCCA ATGAGAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA 148

(2) INFORMATION FOR SEQ ID :1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT 50
 AATCAAGAAA AAATAGCACC AACACAATG AGGAGAAAAT GGAAAAAGGG 100
 CAGAGTATTT CAAAGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT 150
 TAAGCCTTCA GTTGGCCCTG TAAGCAAACCT GAAGACGTGC AAGTCATCCT 200
 TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAAATTA 240

(2) INFORMATION FOR SEQ ID :1121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs

569

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

10	AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG	50
	GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA	100
	AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG	150
15	ATTTTAAAGC CTTACGTCT GCCCTGTAAG CAACTGAAG ACGTGCAAGT	200
	CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGGCA ATGAGAAGGG	250
20	ACAG	254

(2) INFORMATION FOR SEQ ID :1122:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 253 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

	AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC	50
35	NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA	100
	TGGAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA	150
40	ACGAATGATT CTTAAGCCTT CACGTTTGCC CTGTAAGCAA ACTGAAGACG	200
	TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC	250

570

GAG

253

(2) INFORMATION FOR SEQ ID :1123:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

15 AAATGGGGAG AATCAACAGA GCCAAGGAC TAATAAAATT AATGAATCCT 50
GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAAATCCGA GAAAATGGAA 100
AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT 150
20 GATTTTAAAG CCTTCACGTC TGCCCTGTAA GCAAACCTGAA GACGTGCAAG 200
TCATCCTTTG 210

25 (2) INFORMATION FOR SEQ ID :1124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC 50
CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA 100
40 TGGAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC 150

571

AACGAATGAT TCTTAAGCCT TCATGTTTGC CCTGTAAGCA AACTGAAGAC 200

GTGCAAGTCA TCCTTTGGAC CCTGGGAGAG T 231

5

(2) INFORMATION FOR SEQ ID :1125:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

AAGTCCCATC AGCAACCCGT TTTTACCAG ATGCTACTCA AGAATGCGCC 50

20 CGTGGCCCTC CAGTTCCTGC GCACTAAGAG CGTCCCGCT 89

(2) INFORMATION FOR SEQ ID :1126:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA 50

35

ACCAAAACTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC 100

ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT 150

40 ATGCTACTGG ACACATGCCC ACACAATAAT ANTCANRTGT NTYGTTAGGC 200

CTACT 205

572

(2) INFORMATION FOR SEQ ID :1127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

GCAAGGCCTG	CCCGACAACA	CCCTTATTGC	TAAAGTAAAT	AATGNCGCGC	50
GGGGCCTGGA	CCACCCTCTG	GAAGAAGATT	GTACCTTGGA	GCTTCTCAAG	100
TCTGAGGATG	AGGAAGCTCA	GGCAGTGTAT	TGGCGCTTTA	GTATCACATA	150
A					151

20

(2) INFORMATION FOR SEQ ID :1128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

GAGCACCCCA	GCCCATAACA	CAGAACTCGT	CCCCCTACCC	CCCTCAGCAA	50
GCCGGAGAGG	CTAGCCCAAG	TAATCATAAY	AACAGCCGCC	CGAGAGCAGC	100
CCCAGTAGCA	GCCCCATGGC	CGGGCGGAAC	ACCTACATCG	ACAACCTCAT	150
GACAGACGAG	ACCTGCCAGG	ACGCAGCCAT	TGCGGGCTGC	AAGGCCTCRC	200
CCTTCGTCTG	GGCCGCCGTC	CCCGGAGAAA	CGCTCGT		237

40

573

(2) INFORMATION FOR SEQ ID :1129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

GCCTCGTGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG 50
CACCACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT 100
CCTTAAGATC ATCCAATAT AGGATG 126

20

(2) INFORMATION FOR SEQ ID :1130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

30

GCCATCTTCT GTAACAAAT AAATAGTGTC AAGCACTAAA TATATGCATG 50
AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT 100
CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG 150
TTTATTTGCA AGGATTTTTC TTTTCGRGGC GGAGGGGAGA GAAAAGTAAA 200
TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCTT YGTATC 246

40

(2) INFORMATION FOR SEQ ID :1131:

574

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1131:

10 CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA 50
TCCTCTGTCT GACCATGATT TTTTCCCTCA AATACAACCA CTCCTCGACT 100
15 TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAG CTCTTGCACT 150
GTACACTTAG AAGTGTAACA TTAAAGCATT ATAGAGCTAT CTACACACCG 200
ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG 250
20 TGCAGACAGA ACTAAAACCA ACT 273

(2) INFORMATION FOR SEQ ID :1132:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35 GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG 50
TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC 100
CTTAGACATT CTTCCAGGCA GGATCAAACCT CAAAGGAAAA GGAATTTGTG 150
40 AAGCAAACCA TGGCTTTGTC ACAGTAAAGT AATTGTCACT CTCAACCCAG 200

575

AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA 250

AGCCAATGTA TCTGACCCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT 300

5 ATTTCTGTTT GTTAAAAAGT TCAGAATTT 329

(2) INFORMATION FOR SEQ ID :1133:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

CCCCGAGCTA GTTGTCCCGA CCTG 24

20

(2) INFORMATION FOR SEQ ID :1134:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

GAGGATCCAC AAACCATGGA ACACTCTCGC GGCTGCCACT CCCCCATGAC 50

35 CACCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA 100

TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG 150

CGGCCCCCTGC CGGGCACCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT 200

40

CCAGGAATCT CTACCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA 250

576

CCAAACCTCG CCAGAAGGCT TCTTTTCGGG TTGATCGCCA TCTATTY

297

(2) INFORMATION FOR SEQ ID :1135:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15 GCCGCTTTAC TGCTCAGTTC GGAGCTACCG CTTCGAAAGC AACAAAAAAG 50

CNTTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA 93

(2) INFORMATION FOR SEQ ID :1136:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:

30

CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG 50

TTGTGGGAGA TAACGGTGGC ATAGTTCCCT GATGCCCGGG CCAGCTTGCC 100

35 ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA 150

TGGTGCCAC AGGGAGCRCA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG 200

CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC 250

40

CGCCCGCTTC TTAAACCAAG ACAGATCCCG GAAGGCCGCC TGGGCAAGGG 300

577

GCCCCCTCRAA CCCGGGGCTA TACACGTCAA AATC

334

(2) INFORMATION FOR SEQ ID :1137:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15 CGAGGATCCG CATACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG 50
ATGAAGAAAC TCCAAACCCT TTGACAGCTC CTCGGGGTNA AACCTGGNAY 100
AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT 150
20 CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT 199

(2) INFORMATION FOR SEQ ID :1138:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35 CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCGAGCGC CGCTCCGCGT 50
GGCACCCGGC TCGCTCCGAG TTTCAGGCTC GTGCTAAGCT AGCGCCGTCG 100
TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC 150
40 ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG 200

578

TTGTGCCTGG AGGTGAAGGG GAAGATGATC AGTAGGACAG AAGGTAACAT 250
TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG 300
5 AAGG 304

(2) INFORMATION FOR SEQ ID :1139:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

GAGGATCCGG GTACCATGAG AAACTTTGAA GCCAGAGATT TTAAACAATC 50
20 AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAAACAAA 100
CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC 150
25 CTTTAATAGT TATCTAAATG CAGAGTTTGT TTATGAAATG AACCAAAGCA 200
GTTTGTCAAT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC 250
CACTACTGGC TAAAGAAACT AAGTAAA 277

30

(2) INFORMATION FOR SEQ ID :1140:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

579

CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCCAA 50
AAGAGAGCTC CCTGAGAAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT 100
5 TTTAGCAGAG CAAATTTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG 150
GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAGTTCA GACTGGGCTC 200
CAGCTTCT 208

10

(2) INFORMATION FOR SEQ ID :1141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG 50
25 CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG 100
TCAACAATGG TTAAGTTTCTAG CCGTACATTG CTTTCCTGAA GCTCATAACT 150
TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACTTT 200
30 TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT 250
GTCTCACCAA TACAAAGGAT GTTG 274

35

(2) INFORMATION FOR SEQ ID :1142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

580

(xi) SEQUENCE DESCRIPTION: SEQ ID :1142:

GCCTGCACAT TGA CTGTGGG AACTCGGAA ACAAGCTCAC ATCTCCCCGT 50
5 GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAAGT CAGTTGCCAC 100
CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTCTGC ATTCCCTTCA 150
10 TTTCTCCTAA AAGATGGCAG AAGATTTTAA AGTCCCGGCT GATGGAGTTG 200
TTAGTGTCTT ATGGTAACAC CTTCTT 226

(2) INFORMATION FOR SEQ ID :1143:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

25

RGGRTCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC 50
TGRRCGNTG NCNGTGAGGR CRTGNRGGNC CRTGCGAGTG GGCTTACCGN 100
30 TAGGTTCGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG 150
GNANGRTGNN GTGGAGRG 168

(2) INFORMATION FOR SEQ ID :1144:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

581

(xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT 50
5 TCTTGAGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTTGC 100
CAGGATTTGA GGAAATCGAC TGCCTTCACT CTTCCCTGAA ACTTTGAAGT 150
CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT 200
10 AAACAACCTT ATAGTGTTTT CGCTTTGAAT TGTATGAATT CTTAGAACTG 250
AGAAGT 256

15 (2) INFORMATION FOR SEQ ID :1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

AAACACAAGG CTAAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA 50
GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG 100
30 TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT 150
GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG 184

35 (2) INFORMATION FOR SEQ ID :1146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

582

(xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

5 CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG 50
CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG 100
ATTTCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT 150
10 TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG 200
GTGCTGAGAA GAATGCACAA G 221

(2) INFORMATION FOR SEQ ID :1147:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

25

CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT 50
TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT 100
30 TAAGGATTCT CACATTCAGG ACAGAGAACA AATTTTTTAA TGAATCCATC 150
CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC 200
RRTMATTCTT AACANCAAAC NGMGMTGNN NTCCCRNCTT ATAACCMAAA 250
35 GATNT 255

(2) INFORMATION FOR SEQ ID :1148:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
(B) TYPE: nucleic acid

583

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:

CGAGGATCCA GGTACCATGG ACGATTCACA GCCCCTGGCC ACTGGCCATT 50

10 TCCAGTGGTA GGGAGCACAC TGRTACATT CGAGACCCAC CACGTTGAGC 100

AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC 150

CCCAGGATGT TGTAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG 200

15

AGTCGGTGAC GCCCGATTTG GATCGGGTGT 230

(2) INFORMATION FOR SEQ ID :1149:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

30 GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA 50

GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTGAGACG TTCTCCTTTC 100

AGGCAGAAAT CGCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG 150

35

AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT 200

GGACAAAATT CGATATAAAA GCT 223

40

(2) INFORMATION FOR SEQ ID :1150:

(i) SEQUENCE CHARACTERISTICS:

584

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1150:

10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC	50
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGATTC CTAATGCCCT	100
	ATGATCACGT GGAAC TAACA TCAATGACA TGAAGAACGT GCCAGAAGCC	150
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	200
	CTTTATGTCC AAGAACAAGG ATGCGATGGG TATTTCTGTA NGCTATTGA	250
20	NMTRAGGRMA GNCTGNAAGG TM	272

(2) INFORMATION FOR SEQ ID :1151:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|----------------------------|
| 25 | (A) LENGTH: 140 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1151:

	TGAGGATTTA TAGATTANAG CTAGAGTTCA CATTTTATGG ATTACAACCA	50
35	AAAAAACCT GAAAAAGAAA AAAACAAAA AAGCTCAAAA GCAATCACAA	100
	GGATAGTTGA ATCCCTCTTT AAACCCCCAA AGCAACCCCC	140

40

(2) INFORMATION FOR SEQ ID :1152:

(i) SEQUENCE CHARACTERISTICS:

585

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1152:

10	AAGGATCCGG GTACCATGTA TTCCCCCGGT ATCAGCAGAG GCGTGTACGG	50
	GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGAGG	100
	GTCACCAAGG TAGATTTCCA GCAGCCTAGT CCAGCTGAAC GCTTTCCAGC	150
15	CTTGCTTTTT AGCAGCTTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC	200
	TTTCATTG	208

(2) INFORMATION FOR SEQ ID :1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1153:

30	CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCCTGGA	50
	TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG	100
35	CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACTCCAG	150
	GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG	200
40	GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA	250
	GAMGCCNMAC AGGGCTRGGG ACTG	274

586

(2) INFORMATION FOR SEQ ID :1154:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1154:

GAGGATCCAC CGACCATGGA ACACTCTCAA TGGCTGCAAC CACCCCGTGG 50
15 CCCCCCTACC AGCCCCAATC TCAAACCCC GCACGTCGAT CATGACGCCA 100
CCAACAGCTG CAGCCCCTGA GATCTTCACC TTAGACCCTC TCCCGAAGCC 150
CGCAGCCGCC CCTGCGAACC CTCCAAC TCG TTCACACGCG CCGAAAGCCT 200
20 ATTCCAGGA CTCTCTGCCC CTACGTGACC GNCCCTAGCT GCTAGTCGAG 250
AATCCGAACT CCGCTCC 267

25 (2) INFORMATION FOR SEQ ID :1155:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

CTCAAACCCC GNTTCCCCC TAATAAGAGC AACTAAAAA CTTCTGATAA 50
CCACAATAAA AGCGTGCATT TGAGCACAAT TCAAAGCCA ACCCCTTCGA 100
40 AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG 150

587

CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC 200

CGTCTANCAA GGCAACGGCC GCCTTTGAAT T 231

5 (2) INFORMATION FOR SEQ ID :1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

GCGCGAGCAC AGAGCCTCGC CTTGCCGAT CCGCCGCCCA TCCACACCTG 50

20 CCGCCAGCTC ACCGTGTATG ATGATATCAC CNGCTCGCC ACCAACRACG 100

GCTCYAACMT GTGCAAGGCC GCCTTCAA 128

(2) INFORMATION FOR SEQ ID :1157:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

35 GCCGCAACAC AACCCAGGGA GACTCAAGNC CACAGGGGCC CCCC GGCTCT 50

GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCCAACA AGGGCAGAAA 100

40 GGTGAGCCTT ATGCACTGCC TAAAGA 126

(2) INFORMATION FOR SEQ ID :1158:

588

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

10

AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA 50

CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAAA AACCCCTCCT 100

15

T 101

(2) INFORMATION FOR SEQ ID :1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG 50

30

GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC 100

CCCACACACG GTGGCGGTGC GGTGAACTG GAAGGGGAGG TCGAAGGTGC 150

35

CATCTTCTTC AGGCCCTCC AC 172

(2) INFORMATION FOR SEQ ID :1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

40

589

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA	50
TGGTTATTTC CCAGGACCAC ACGATTGCCC TACGTCCTG GAAGGCTATG	100
10 TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG	150
CTTTGACCCT GTGATGCCAT TTAATCAAC CCTGCTTGGT TTTAGAGGAT	200
15 TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT	235

(2) INFORMATION FOR SEQ ID :1161:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG	50
30 TTAGATACAA ATGCAAAACG CTCCTAAAA AACGGCCTGA AAAAAAATC	100
ACAGACAATG CCAAACCTTA TAGGTCTGTA TTTTCCTTTA TACAAAATGC	150
35 CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG	200
ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA	250
ACCCTCATAA AGCCTTAAAA GTACATTTGT GAAA	284

40

(2) INFORMATION FOR SEQ ID :1162:

590

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

10

GCTCACATAA ATTTCTTCAC CGACCCTTTT CCTTCCAGCT TCCTTACTAT 50

AAAAAACCCC ACA AATA TGTTTCATCAT CATCCATACT AACCAACCCC 100

15

GTCACCATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAACCTTG 150

TTACCACCTC TAGGGGCAGA CCCCTTTTCA GATATATTCA AGAGTTTAAT 200

ATCCTCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA 250

20

ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC 287

(2) INFORMATION FOR SEQ ID :1163:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

35

GAGGATCCAA AAACCATAAA ATTCATCATC CCCAGCAGGT GCNCTAGCTA 50

TACTTTATTA CAGCAAARCA CAACCACACG CTGAMCTANM TCGTATAGAT 100

AAACACCAAT CATGGGTCGG CC 122

40

(2) INFORMATION FOR SEQ ID :1164:

591

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1164:

10

GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG 50
GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCTCTC CACTTGCAAC 100
CTCCAAGACC ATCTTCTCGG CCATCTCTG CTCTGAAGC CT 142

(2) INFORMATION FOR SEQ ID :1165:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

TATTCCTCCG GTATCAGCAG AGGCGGTGAC GGGCACTGCT TTAAACTGG 50
GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC 100
CAGCAGCCCT AGTCCAGCTG AACACTTTCC AGCCTTGCTT TTCAGCAGCT 150
TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG 200
GATGAGAATA GAGAACTCA 219

(2) INFORMATION FOR SEQ ID :1166:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs

592

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:

GAGGATCCAC CAACCATAGA AAGGAAACAA CACTTGGAGT GAACCCGACC 50
10 CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA 100
AACAACCGGA AAATAGACCC GGACGAAGAT CAAAGTTTNT CAATCCAAAC 150
15 ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC 200
AA 202

(2) INFORMATION FOR SEQ ID :1167:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:

30

GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAAATG ACCTTTACGA 50
AGACACGTCT GATACCCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG 100
35 GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC 150
ATCTGGAGA 159

(2) INFORMATION FOR SEQ ID :1168:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs

593

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1168:

CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG 50
10 CGATTGCCAC CGCTTCTCTC TAGTCTCAGG AGGGGTTTCC CGCCTCGCAC 100
CCCCACCTCT GGAATTGCCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC 150
15 CAGCGCTTAG GTCGGAGCGA GCCTGGGGCC ACCGCCGTGA AGACATCGCG 200
GGGACCGATT C 211

20

(2) INFORMATION FOR SEQ ID :1169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1169:

GGATTTCCGG TCCTGGCTTT CTGATATTTC TAAATCGAC CTGGAATCAA 50
CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC 100
35 CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT 150
TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG 200
ATGAACACTT T 211

40

(2) INFORMATION FOR SEQ ID :1170:

594

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10 GAGGATCCGC GCAACCATAG AACTCACAAC CCAGCCATAT ACCTCAGACA 50
CAATGGAATG GGCGGAGGTC GAGGTNGACA AACCTGAGT AATGTTGGGC 100
15 ACTTCCGCAC CGGAGCTGTT CTTACCTTTG ATAAAGTGA TGTATTGCT 150
ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC 200
CTATCCACCA ACGNCGAACA ATATGCTGTT GCCAMGATTG AGCACGAGCC 250
20 GTTTGGGCTC AACGGC 266

(2) INFORMATION FOR SEQ ID :1171:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35 GGCACAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG 50
CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG 100
GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTTGAGGGC 150
40 TTTAATCCTT TAAAACT 167

595

(2) INFORMATION FOR SEQ ID :1172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC 50
TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG 100
ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT 150
TACTGAGGAT ACGCAACTCA TAAAACTCTA CTAAAGCAA CAGGGCAGAC 200
GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC 232

20

(2) INFORMATION FOR SEQ ID :1173:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT 50
CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC 93

40

(2) INFORMATION FOR SEQ ID :1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs

596

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

GCCTTTTTTT	ACCCGCCGGA	AGCTACAGCT	TTTGCCCCC	CAAAAAACC	50
10	CCACCCTTTT	ACCCACCGCG	GACCCAAAAA	CAGCAAAAC	100
	CAAGGACCTC				
	TCCCAACCCC	AACCCCTCCT	TTTTGGCCCT	TCCTTCCCCC	150
15	CACCCCCAGA	CACCTCAATC	CCCCAAAAGG	ATGCCCTAAA	200
	CCTCTCTTAA				

(2) INFORMATION FOR SEQ ID :1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

GAGGATCCAA	AAACCATGGC	ATTCATCACG	CCCAGCAGGT	GTCCCAGCCA	50
30	TGACTTACCA	TAGCAAAACA	CAACCACACA	CTAACCTGCA	100
	TCGCCTAGCT				
	TACTGATGAT	GATGTCCTGG	T		121

(2) INFORMATION FOR SEQ ID :1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

597

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC

26

5

(2) INFORMATION FOR SEQ ID :1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG

50

20

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT

100

CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT

150

TCAGGATGGA TTMAAGNAMG CAGAGAGG

178

25

(2) INFORMATION FOR SEQ ID :1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA

50

40

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCACAG TTTGCCCGTG

100

TGTTATGCAT CAGTTATACA GGTATCCAC CAAGTTCAAG TCAA

144

598

(2) INFORMATION FOR SEQ ID :1179:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

GACCAGGGAG GAGGTTTAAT CAACTTGGAC CCCCTCCGGC CTAGCCGCCG 50
15 AGGAGGTGCA TTCGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG 100
TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCAGCT TTGATTTACT 150
GATCTCGCTG AAAAGACAGA CGCTTTTAGA TACCGAGTCG ATAGGGGGTC 200
20 TGCGGTACTT TTCAGTAGAT AGGTGGTGCT TGT 233

(2) INFORMATION FOR SEQ ID :1180:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

35 CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC 50
CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA 100
TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCGCCC GAGCCCCCTT 150
40 CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG 200

599

AGGTAGACGG GACCAAGATC TGCTG

225

(2) INFORMATION FOR SEQ ID :1181:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15 TGAGGATTTA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC 50
GATGAATAAG CTTCATGTGG CCTAGTTTTN NGNNNNNTGG NYATGGTNNA 100
TCNNNTTANT TTTTGGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG 150
20 TTTAGAGTTT GGAAGCGGCN RNCCTARMG NNACTCYACG CTCGCNNCTN 200
TTGNNNNACA GMRGGNTCTC TNGGRTGAGT GGRINCMGTT GGMGGNNTCN 250
25 NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTNGGCTN GCT 293

(2) INFORMATION FOR SEQ ID :1182:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

40 GAGGATCCGG GTACCATGGC TCTCTCTTC TTTTTTCT TTTTCTGGC 50
GGATGTGAGA GCTGCCTGAG ATTCAAGGC ATCCGGCAGC TCAGTCCCCA 100

600

CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTTCTCA 150
GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCATTCC 200
5 TTCTGGCTGT TGAGACCCCG TGGACTCCCC TGGATTCCAG AGNNTNATTT 250
NG 252

(2) INFORMATION FOR SEQ ID :1183:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

20

ACGAGGATCT GAATACTCTG GCCTGCAACT AGAGGCTAAT TCGATGTGTG 50
AAACTGTAGA TTCGGCTTAA GGTAATAGTC ATTTATAGAC TATTCAATAG 100
25 AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT 150
ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT 200
GT 202

30

(2) INFORMATION FOR SEQ ID :1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTTCGTGG TTCACAATTT CTCAGTCTC TTA

43

(2) INFORMATION FOR SEQ ID :1185:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

15 ACCGTCCTTC TGGTTCATCC TAGCAAAAT CTCACCATCT TCTATCAC

48

(2) INFORMATION FOR SEQ ID :1186:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

ACATCATCCG AGTCCCCTCT ACAGTGTTCA TTGTGATCGT TGCATCCCCC

50

30

TGGTTTGAA ATAAATATA AACTGCCCGG CAAGAGATAA AATTGTATTT

100

TTTA

104

35 (2) INFORMATION FOR SEQ ID :1187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

602

(xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG 50
5 AGAATCCTAT TCAGTGCTCC CTTAGA 76

(2) INFORMATION FOR SEQ ID :1188:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

20 AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA 42

(2) INFORMATION FOR SEQ ID :1189:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

GGCGGACGTG CGCGCCTTGT CTTGCGGCA CCTGGGCCTG AGGTGCGTGC 50
35 CTCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC 100
GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC 150
40 GCCAAGGCCT TTTATTTATG GCTAGTTTGC TCTCGTGAAA TACTAACATC 200
GTTTAAATGG CACTCATCAA GTACGCAAAT GATATGATTT AACCTCGCGC 250

603

AAT

253

(2) INFORMATION FOR SEQ ID :1190:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15 GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG 50
TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA 100
CAACTACTCC AATTGCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT 150
20 GAATTTAGGT TGGTTACCAA TATCGGCATA AAATAAACTR TGTAAGGCTC 200
AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT 250
25 TT 252

(2) INFORMATION FOR SEQ ID :1191:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

40 GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCCAAC GATCTAACTA 50
ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC 100

604

TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TGCCAACCA 150

CCCTTCCGGC TGCCCTTGTG TTGACTTG 178

5 (2) INFORMATION FOR SEQ ID :1192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCGG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT 50

CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT 100

20 GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNG 150

NGGGCA 156

25 (2) INFORMATION FOR SEQ ID :1193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTGTG AATACAGACA 50

TAACTGCAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA 99

40

605

(2) INFORMATION FOR SEQ ID NO: 1194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

NNNNTCCTTC TCCTGCGACA GACA

24

15

(2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

TGTCTGTCGC AGGAGAAGGA

20

30

(2) INFORMATION FOR SEQ ID NO: 1196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:

AANNTCTCGG ACAGTGCTCC GAGAAC

26

606

(2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNTCTCGG ACAGTGCTCC GAGAAC

26

15

(2) INFORMATION FOR SEQ ID NO: 1198

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA

22

30

(2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

GTTCTCGGAG CACTGTCCGA GAG

23

607

(2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC

23

15

(2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGTCTGTCG CAGGAGAAGG AA

22

30

(2) INFORMATION FOR SEQ ID NO: 1202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:

CTGTCTGTCG CAGGAGAAGG AG

22

608

(2) INFORMATION FOR SEQ ID NO: 1203

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG

17

15

(2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCC

24

30

(2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:

GATCCGGCTC GAGT

14

609

(2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCG

18

15

(2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAACGAC GGCCAGT

17

30

(2) INFORMATION FOR SEQ ID NO: 1208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:

CGAGGTCGAC GGTATCG

17

610

(2) INFORMATION FOR SEQ ID NO: 1209

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG

17

15

(2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT TTTTTTTTTT

50

TTTTTT

56

30

(2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 11 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:

611

GCCWSCGCCG A

11

(2) INFORMATION FOR SEQ ID NO: 1212

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

15 GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO: 1213

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

30 TTGACACCAG ACCAACTGGT AATG

24

35 In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

40 85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

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10

15

CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-
 - (a) a sequence selected from SEQ ID Nos 1 to 1193;
 - (b) an allelic variation of a sequence as defined in (a); or
 - (c) a sequence complementary to (a) or (b).
2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.
3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.
4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.
5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.
6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.
7. A nucleic acid sequence as claimed in claim 2 or claim 3 and encoding at least a portion of a biologically active polypeptide.
8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.
9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.
10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

614

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a gene.

12. A DNA fragment comprising a gene obtainable by the use defined in claim 11.

13. An expression vector comprising a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a DNA fragment as claimed in claim 12, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

14. A vector as claimed in claim 13, wherein said vector control or regulatory sequence comprises a regulatable promoter.

15. Host cells which incorporate as a heterologous part of their expressible genetic information a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, or a DNA fragment as defined in claim 12.

16. A process for the production of a polypeptide comprising cultivating host cells as defined in claim 15.

17. An antibody directed against a polypeptide obtainable by the performance of a process as defined in claim 16.

18. An antibody as claimed in claim 17 and which is monoclonal.

19. A novel gene product or portion thereof encoded by a fragment as defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as defined in any one of claims 2, 3 or 7, or encoded by the gene comprised in a DNA fragment as defined in claim 12.

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(21) International Application Number: PCT/GB93/01467 (22) International Filing Date: 13 July 1993 (13.07.93) (30) Priority data: 9214857.6 13 July 1992 (13.07.92) GB (71) Applicant (for all designated States except US): MEDICAL RESEARCH COUNCIL [GB/GB]; 20 Park Crescent, London W1N 4AL (GB). (72) Inventors; and (75) Inventors/Applicants (for US only) : SIBSON, David, Ross [GB/GB]; 37 Grimsdells Lane, Amersham, Buckinghamshire HP6 6HF (GB). GROSS, Jacqueline [GB/GB]; 47 Boxmoor Road, Kenton, Middlesex HA3 8LH (GB). HADFIELD, Kathryn, Mary [GB/GB]; 5 Carlisle Terrace, St Ives, Huntingdon, Cambridgeshire PE17 4PQ (GB). HOWELLS, David [GB/GB]; 77 Puttocks Drive, Welham Green, Hatfield, Hertfordshire AL9 7LW (GB). STARKEY, Michael [GB/GB]; 27 Creasy Close, Abbots Langley, Hertfordshire WO5 0HS (GB). KELLY, Maria [IE/GB]; 24A Oxford Road, Ealing, London W5 3ST (GB). SHAW, Diana [GB/CA]; 342 Glacier Hall, University of Calgary, 2500 University Drive NW, Calgary, Alberta T2N 1N4 (CA).		(74) Agent: BIZLEY, Richard, Edward; Hepworth Lawrence Bryer & Bizley, 2nd Floor Gate House South, West Gate, Harlow, Essex CM20 1JN (GB). (81) Designated States: AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 31 March 1994 (31.03.94)
(54) Title: HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW (57) Abstract <p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>		

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ES	Spain			VN	Viet Nam
FI	Finland				

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/GB 93/01467

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all) ⁶		
According to International Patent Classification (IPC) or to both National Classification and IPC Int. Cl. 5 C 12 N 15/11 C 12 N 15/62 C 12 P 21/08 C 07 K 15/28 C 12 Q 1/68		
II. FIELDS SEARCHED		
Minimum Documentation Searched ⁷		
Classification System	Classification Symbols	
Int. Cl. 5	C 12 N C 12 Q C 07 K	
Documentation Searched other than Minimum Documentation to the Extent that such Documents are included in the Fields Searched ⁸		
III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹		
Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
Y	SCIENCE vol. 252, 21 June 1991, LANCASTER, PA US pages 1651 - 1656 ADAMS, M. ET AL. 'Complementary DNA sequencing: expressed sequence tags and human genome project' see the whole document ---	1-19
Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA vol. 88, March 1991, WASHINGTON US pages 1943 - 1947 PATANJALI, S. ET AL. 'Construction of a uniform-abundance (normalized) cDNA library' cited in the application see the whole document ---	1-19
-/-		
<div style="display: flex; justify-content: space-between;"> <div style="width: 45%;"> <p>¹⁰ Special categories of cited documents :</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="width: 45%;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"A" document member of the same patent family</p> </div> </div>		
IV. CERTIFICATION		
Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report	
08-10-1993	01. 02. 94	
International Searching Authority	Signature of Authorized Officer	
EUROPEAN PATENT OFFICE	ANDRES S.M.	

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category "	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
Y	NUCLEIC ACIDS RESEARCH vol. 18, no. 19, 11 October 1990, ARLINGTON, VIRGINIA US pages 5705 - 5711 KO, M.S.H. 'An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs' cited in the application see the whole document ---	1-19
Y	NATURE vol. 355, 13 February 1992, LONDON GB pages 632 - 634 ADAMS, M. ET AL. 'Sequence identification of 2,375 human brain genes' see the whole document ---	1-19
Y	GENE vol. 81, 1989, AMSTERDAM NL pages 295 - 306 AKOWITZ, A. & MANUELIDIS, L. 'A novel cDNA/PCR strategy for efficient cloning of small amounts of undefined RNA' see the whole document ---	1-19
P,Y	WO,A,9302214 (MEDICAL RESEARCH COUNCIL) 4 February 1993 see the whole document -----	1-19

INTERNATIONAL SEARCH REPORT

International application No.

PCT/CIB93/01467

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos. ...
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos. ...
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos. ...
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see PCT/ISA/206 mailed on 29.11.93

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-19(all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.**

**GB 9301467
SA 76316**

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EIDP file on 02/02/94
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A- 9302214	04-02-93	None	

EPO FORM P079

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82